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Contact: George J. Kargul Laboratory of Genetics National Institute on Aging/National Institutes of Health 33 Cassell Drive, State 400, Baltimore, MD 21224-6820, USA		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus REFERENCE 1 (bases 1 to 673) AUTHORS Karqui.G.T. Dudekula D.B. Otan v. Virtus V. Tarakina.	VERSION BG071693.1 GI:12554262 KEYWORDS EST. SOURCE house mouse. ORGANISM Mus muscullus	DEFLICATION (BG071693 ACCESSION (BG071693 ACCE
Contact: George J. Kargul Laboratory of Genetics National Institutes of Health National Institutes of Health 33 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov This Clone set has been freely distributed to the community. Please visit htry.//fcus	of NIA mouse 15K cDNA clone set	ata; Vertebrata; Euteleostomi; ognathi; Muridae; Murinae; Mus.		mRNA linéar EST 26-JAN-2001 Set Mus musculus cDNA clone

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978. "
191 c 173 g 172 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          )-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryousing a 15,000 mouse developmental cDNA microarray, 2000. Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NIA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
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URL:http://genome.gsc.riken.go.jp,
Carninoi,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninoi,P., Shibata,Y., Muzamatsu,M. and Hayashizaki,Y.
M., Konno,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
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Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN Mouse ESTs (Arakawa, T., et al. 2001) Unpublished (2001)
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                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                               encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
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                                                                                            further details
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                                                                                                                                                                                                                                                                                                                                                                                        Computer-based methods for the mouse full-length cDNA
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                                                                 e mouse tissues.
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smooth, rukunishi, K., Shibata,K., Itoh,M., Carninci,P., Sugahara
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                              Location/Qualifiers
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/organism="Mus musculus"

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Matches 660;
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                                                              766 AGCACGGAGGAGAAGGAGCGCCTGCGTTTCGAGTTCTTAGAGCAGAAGTACGGCTAC 825
                                                                                                                                                                                                                                                                         706 GCAGAGATGGCTCAGGACCCCGGTGATTCGGATGCCCCCTCGAGACCAGGCCTCCCCGCAA 765
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/dev_stage="10 days neonate"
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                                                                                                                                                             cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1727-1771 (2000) Konno, H., Fukunishir., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carrinci.P., Shibata,Y., Hayatsu.N., Sugahara,Y., Shibata,K., Itoh
Normo,H., Okazaki.Y., Muramatsu.M. and Hayashizaki.Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi.K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki.M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
                                                                                                                                                                                                                                                                                                                                                                                                                                  encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Alzawa K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                   prepare mouse tissues
                                                                                                                                                                                                                                                                                          Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                              Human Genome Sequences Mamm.
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Hiramoto, K., Hori, F., Ishil, Y., Ito, M., Kawai, J., Konno, H., Kouda
, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Okido, T., Saito, R., Sakai, K., Saho, H., Sasaki
, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
                                                                                                                                                                                                                                                                                                                                              Computational Analysis of Full-Length Mouse cDNAs Compared with uman Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/clone="A830014H23
                                                         /organism="Mus musculus"
                            /db_xref="taxon:10090"
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1068 AACGCCTGTCCTGCGACAGCACCTTCAGCTTCAAATACATCATTTAGTGAGAGTCGAAAA 1127
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                             TCCCTTTCCAAATTCTTCATGACAGACAGTGTTACTTGGATATAAAGCCTGTGAATAAAA 1247
                                                                                                                                             CGTTTCTGCTAGATGGGCTAATGGAATGGACAAGTGAGCTTTCTCCCCCTCTTCACCTCT 1187
                                                                                                                                                                                                                                                                                           TCCCTTTCCAAATTCTTCATGACAGACAGTG-TACTTGGATATAAAGCCTGTGAATAAAA 658
                                                                                                   CGTTTCTGCTAGATGGGGCTAATGGAATGGACAAGTGAGCTTTCTCCCCTCTTCACCTCT 599
                                                                                                                                                                                               AACGCCTGTCCTGCGACAGCACCTTCAGCTTCAAATACATCATTTAGTGAGAGTCGAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper cDNA went through one round of normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RIKEN full-length enriched, 10 days neonate cortex" \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified pBluescript KS(+) after bulk excision from Lambda
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GAGAGAGAGAGAGCTCTTTTTTTTTTTTTTTTTVN 3'), cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer (5' \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="10 days neonate"
/lab_host="DH10B"
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512 CGGCATCCTCGGGGACCCGGGAACCGGAGCCGAGAGGAGGTGGCCGCGAGGAAAGCGGTCC 571
                                                                     Local Similarity
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H3102B03 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details. plate: H3102 row: B column: 03
Seq primer: -21M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: George J. Kargul Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Verifieetton and initial annotation of NIA mouse 15K cDNA clone set
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Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka,T.S., Carter,M.G. and Ko,M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other Bons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Vector: psport]; Site_1: Sall; Site_2: NotI; This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryo from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb: All
                                                                                                                                                                                     patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978.
                                                                                                                                                                                                                                                                                                                             )-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryousing a 15,000 mouse developmental cDNA microarray, 2000 Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                  source libraries are cloned unidirectionally with Oligo(dT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NIA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
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99.7%;
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CDNA Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose
availability will be considered under appropriate and limited
             collaborative arrangements
Seq primer: M13 Reverse.
                                                                                                                                                                                                            Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF471866 594 bp mRNA linear EST 04-DEC-:
UI-M-BH3-awu-b-08-0-UI.rl NIH_BMAP_M_S4 Mus musculus cDNA clone
UI-M-BH3-awu-b-08-0-UI 5', mRNA sequence.
                                                                                                                                                             Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                                                                                                                                                                                         Genome Res. 6 (9), 791-806 (1996)
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                                    GTAAAAGAACTAGATGTGCCTGCCCAGTCAGATTTCGCCACGTGGACCCTAAACGCCCCC 1034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 5:791-806, 1996)*

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Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Inotani, K., Ishii
Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Inotani, K., Ishii
N., Y., Ito, M., Kawai, J., Kojima, Y., Konoo, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinaqawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Tagawa
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A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hansehiaria v
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing pipeline with 384 multicapillary sequencer. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                     further details
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/db_xref="taxon:10090"
/clone="7420459B08"
/tissue_type="in vitro fertilized eggs"
/dev_stage="egg"
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/sex="female"
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                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                              /clone_lib="RIKEN full-length enriched, in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              525 bp
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                                                                                                                                                                                                                                                                                                                                                         1032 CCCATCGGCAAGACTTGTGTGGGAGATGCAAGGACAAACGCCTGTGCTGCGACAGCACCT 109:
                                                                                                                                                     1152 GAATGGACAAGTGAGCTTTCTCCCCTCTTCACCTCTTCCCTTTCCAAATTCTTCATGACA 1211
                                                                                                                                                                                                                                 1092 TCAGCTTCAAATACATCATTTAGTGAGAGTCGAAAACGTTTCTGCTAGATGGGGCCTAATG 1151
                                                      1212 GACAGTGTTACTTGGATATAAAGCCTGTGAATAAAAGGTATTGCAA 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       852 GTGGGAGAGCGCCTATGTGTGGTGTGTGCAGGGCACCAGTAAGGTGTTACTTCAAACAGT 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   732 TTCGGATGCCCCTCGAGACCAGGCCTCCCCGCAAAGCACGGAGCAGGACAAGGAGCGCCT 791
     480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     912 TCTGCCGAGTGTGTGAGAAATCCTACAACCCTTACAGAGTGGAGGACATCACCTGTCAAA 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   972 GTTGTAAAAGAACTAGATGTGCCTGCCCAGTCAGATTTCGCCACGTGGACCCTAAACGCC 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 TCTGCCGAGTGTGTGAGAAATCCTACAACCCTTACAGAGTGGAGGACATCACCTGTCAAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                  240 GTTGTAAAAGAACTAGATGTGCCTGCCCAGTCAGACTTCGCCACGTGGACCCTAAACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TTCGGATGCCCCTCGAGACCAGGCCTCCCCGCAAAGCACGGGGCAGGACAAGGAGCGCCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGTTTCCAGTTCTTAGAGCAGAAATACGGCTACTATCACTGCAAGGACTGCAAAATCCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGTTTCCAGTTCTTAGAGCAGAAGTACGGCTACTATCACTGCAAGGACTGCAAAATCCG 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGGGAGAGCGCCTATGTTTGGTGTGTGCAGGGCACCAGTAAGGTG-TACTTCAAACAGT 179
GACAGTG-TACTTGGATATAAAGCCTGTGAATAAAAGGTATTGCAA 524
                                                                                                    GAATGGACAAGTGAGCTTTCTCCCCTCTTCACCTCTTCCCTTTCCAAATTCTTCATGACA
                                                                                                                                                                                                           TCAGCTTCAAATACATCATTTAGTGAGAGTCGAAAACGTTTCTGCTAGATGGGGGCTAATG 419
                                                                                                                                                                                                                                                                                                                CCCATCGGCAAGACTTGTGTGGGAGATGCAAGGACAAACGCCTGTCCTGCGACAGCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-*Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research forcup in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5^\prime]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primed with a primer [5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 497.2; DB Pred. No. 6.1e-77
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DEFINITION
                                                                                                                                                                                        AI854700/c
                                                                        KEYWORDS
                                                                                              VERSION
                                                                                                               ACCESSION
                                                                                                                                                                      COCUS
                                     ORGANISM
                                                                                                         UI-M-BHO-akc-d-12-0-UI.S1 NIH_BMAP_M_S1 Mus musculus cDNA clone UI-M-BHO-akc-d-12-0-UI 3', mRNA sequence.
                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                              AI854700.1
                                                        house mouse
                                                                                              GI:5498606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
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                                       source
                                                                                                                                                                                                                                                                                         379
                                                                                                                                                                                                                                                                                                           892 AAGGTGTTACTTCAAACAGTTCTGCCGAGTGTGTGAGAAATCCTACAACCCTTACAGAGT 951
                                                                                                                                                                                                                                                                                                                                                                                                                499 GAGCAGGACAAGGAGCGCCTGCGTTTCCAGTTCTTAGAGCAGGAAGTACGGCTACTATCAC 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               772 GAGCAGGACAAGGAGCGCCTGCGTTTCCAGTTCTTAGAGCAGAAGTACGGCTACTATCAC 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                             CCACGTGGACCCTAAACGCCCCCATCGGCAAGACTTGTGTGGGAGATGCAAGGACAAACG
                                                                                                                                        GGAGGACATCACCTGTCAAAAGTTGTAAAAATAACTAGATGTGCCCTGCCCAGTCAGACTTCG
                                                                                                                                                                                                                                                                          AAGGTG-TACTTCAAACAGTTCTGCCGAGTGTGTGAGAAATCCTACAACCCTTACAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized basal ganglia library cDNA Library preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. Seq primer: M13 Forward POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, 20892-9643, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Chin, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          discovery
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Bonaldo, M.F., Lenno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="27-32 days"

/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/note="vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The Not I; Site_2: Eco RI; The Not I; Site_3: Eco RI; The Not RI; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/Clone="UI-M-BH0-akc-d-12-0-UI"
/Clone_lib="NIH_BMAP_M_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAG_TISSUE=basal-ganglia
TAG_SEQ-TGTAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAG_LIB-NIH_BMAP_M_S1
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99.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 473.8;
Pred. No. 7.
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FEATURES
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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e mouse tissues.
                                                                                                           encyclopedia: real-time sequence clustering for construction nonredundant cDNA library. Genome Res. 11 (2), 281-289 (200
                                                                                                                                                                                                                             RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugaharu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, JarTel: 81-45-503-9222 Fax: 81-45-503-9216
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Contact: Yoshihide Hayashizaki
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="7420449J15"
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/tissue_type="in vitro fertilized eggs"
/dev_stage="egg"
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S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
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Fax: 81-45-503-9216
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jan
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                                                                      prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
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                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="egg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fertilized eggs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                       /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="in vitro fertilized eggs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="7420466L07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B"
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                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 436)

Ko,M.S.H., Kitchen,J.R., Wang,X., Threat,T.A., Sun,T., DePalma,G.E., Liang,Y., Kargul,G.J., Sharara,R., Lim,M.K. and Doi,H.
Systematic analyses of genes expressed in 16-cell mouse embryo (The ERATO/Doi Project at Wayne State University)
                           Doi Bloasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Ch
                                                                                                                                                                                                                                                                                               AU044294 Mouse sixteen-cell-embryo cDNA Mus musculus cDNA clone 30917609 3', mRNA sequence.
Email: hd@bioa.jst.go.jp.
Location/Qualifiers
                                                                                                Unpublished (1998)
                                                                                                                                                                                                                             Mus musculus
                                                                             Contact: Hirofumi Doi
                                                                                                                                                                                                                                                                           AU044294.1 GI:3979844
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                                                                                                                                                                                                                                                                                                                                                                                             136 GAAAACGTTTCTGCTAGATGGGGCTAATGGAATGGACAAGTGAGCTTTCTCCCCTCTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               424;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 425)
                                                                                                                            BB705931 RIKEN full-length enriched, in vitro fer musculus cDNA clone 7420484F16 3', mRNA sequence.
                                                          Mus musculus
                                                                                              EST
                                                                                                         BB705931.1 GI:16054766
                                                                                                                                                                              BB705931
                                                                              nouse mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 3/j; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="sixteen-cell-embryo"
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bonaldo.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="J0917G09"
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97.0%;
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Pred. No. 5e
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AUTHORS

Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T. Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, F.

Imotani, K., Ishii

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COMMENT
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Matches 422;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
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URL:http://genome.gsc.riken.go.jp/
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The Institute of Physical and Chemical Research (RIKEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computer-based methods for the mouse full-length cDNA
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Conservative
                                                                                                                                                                prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="7420484F16"
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the Not I and Eco RI sites of
             T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into
                                                        primer
                                                                                             /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                     /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                          450 bp mRNA linear EST 03-OCT-: UI-M-BH3-awu-b-08-0-UI.sl NIH_BMAP_M_S4 Mus musculus cDNA clone UI-M-BH3-awu-b-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                            Mus musculus
                                                                         6001 Executive Blvd. 20892-9643, USA
                                                                                        National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC
                                                                                                                                                                                 discovery
                                                                                                                                                                                                               1 (bases 1 to 450)
Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                      BE946858
                Email: mEST@mail.nih.gov
                                                                                                                              Contact: Chin, H
                                                                                                                                                              Genome Res. 6 (9),
                                                                                                                                                                                                  Normalization and subtraction: two approaches
                                                                                                                                                                                                                                                                                                                                                 BE946858.1 GI:10524617
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301 443 9890
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   track not found,
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133 c
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86.1%;
                                                                                                                                                                                                                     Lennon, G. and Soares, M.B.
                                                                                                                                                                791-806 (1996)
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beginning of sequence
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CGGGCGCCGCACGCTGCAGCCTGCAGGGTGCCGAGCCCAGCCCCGACGCCCGATCGGGTTC

CAGCCGTGACGCTGCGGTGCAGGTGAACCCGCGCCGCGACGCCTCGGTGCAGTGTTCACT

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FEATURES
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CAGCCGTGACGCTGCGGTGCAGGTGAACCCGCGCGCGGACGCCTCGGTGCAGTGTTCACT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCTTATCCGCAGGCCACCAAAGCCGGGGATGGCTGGAGGTTCGGAGCCAGGGGGCTGCCG 176
                                                                                                                                                                                                                                                                                                                                                            TCCTTATCCGCAGGCCACCAAAGCCGGGGATGGCTGGAGGTTCGGAGCCAGGGGCTGCCG 122
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                                                                                       ACCCGCGCCCCCCTCCTTCCTCCCCCGGCTACAGACAGCTCATGGCCGCGGGAGTACGTCGA 236
                                                                                                                                                                                                                                                                    ACCCGCGCCCCCCTCCTTCCTCCCCGGCTACAGACAGCTCATGGCCGCGGAGTACGTCGA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: M13 Forward POLYA=No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pT/TDD-Pac (Pharmacia) with a modified polylinker; Site1: Not I; Site2: Eco RI; The NIH_BMAP_M_S4 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.2 and NIH_BMAP_M_S3.2 and NIH_BMAP_M_S3.2. and NIH_BMAP_M_S3.3 niH_BMAP_M_S3.2. and NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with a pool of the NIH_BMAP_M_S3.3 niH_BMAP_M_S3.1 libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydravapartite column chromatoraphy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
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168 c 156 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NIH_BMAP_M_S4"
/dev_stage="27-32 days"
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Pred. No. 8.2e-59;
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CGGGCCGCACGCTGCAGCCTGCAGGGTGCCGAGCCCAGCCCCGACGCCCGATCGGGTTC 4.1.6

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RESULT 14
BB704449
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BB704449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanka,T., Matauura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Saito, R., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y., Watahiki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                               encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watahiki,M.,
,S., Kawai,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB704449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                further details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y. and Hayashizaki,Y
                                                                                                                                                                                                                                                                                                                                        e mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Konno, H., Fukunishi, Y., Shibata, K., Itoh, M.,
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81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81-45-503-9216
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RIKEN full-length enriched, in vitro fertilized eggs Mus cDNA clone 7420464A04 3', mRNA sequence.
                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                             /tissue_type="in vitro fertilized
/dev_stage="egg"
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                         /sex="female"
                                                                                                                            fertilized eggs"
                                                                                                                                                      /clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                 /clone="7420464A04"
                                                                                                                                                                                                         /db_xref="taxon:10090"
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
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1014 ACGTGGACCCTAAACGCCCCCATCGGCAAGACTTGTGTGGGAGATGCAAGGACAAACGCC 1073
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 521)
                                                                                 Mus musculus
                                                                                                                                                                                     BB703869 RIKEN full-length enriched, in vitro fertilized eggs Musmusculus cDNA clone 7420457C21 3', mRNA sequence.

BB703869
                                                                                                                                                               BB703869.1 GI:16052704
                                                                                                            house mouse.
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
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 Mismatches

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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
w8gi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
w8gi,K., Fujiwake,S., Inoue,K., Togawa,Y., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
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RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                further details
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The Institute of Physical and Chemical Research (RIKEN)
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                           cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGTCTCGAGTTAATTAATACCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI" a 130 c 119 g 111 t
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/tissue_type="in vitro fertilized eggs"
/dev_stage="egg"
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/strain="C57BL/6J"
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490 -ATACTTGAATATAAAACCTGTGAATAAAAGGT 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following absembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBLE; SW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (07-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBLO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Aug 11, 2002 this sequence version replaced gi:22003146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-384C22 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For firther details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 During sequence assembly data is compared from overlapping clones.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VECTOR: pBACe3.6.
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                                                                                                                                                          RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Sharna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Brown, A., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Landers, R., Jones, C., Machan, J., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Micol, R., Norbu, C., Norman, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Koman, J., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Vench, V., Vill, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Jambek, H., Zimmer, A. and Zodv, M.
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                          Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320-Chartes Street, Cambridge, MA 02141, USA
                                                                                                                            Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., McDau, T., Mlnova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Morbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Stanuss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigillo, J., Vassiliev, H., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainduh, J., Bembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted—221-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Chartes-Street, Cambridge, MA 02141, USA On Apr 21, 2002 this sequence version replaced gi:18308388. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastlen,V., Bloom,T., Boguslavkly,L., Boukhgalter,B., Brown,A., Camaratta,J., Campopiano,A., Chang,J., Chazaro,B., Choepei,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna, Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna, Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna, FitzHugh,W., Gage,D., Galagan, FitzHugh, W., Gage,D., G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by the finished sequence as soon as it is available and the accession number will be preserved.

1 630: contig of 630 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
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Consensus quality: 141008 bases at least 040
Consensus quality: 142434 bases at least 030
Consensus quality: 142434 bases at least 030
Consensus quality: 142970 bases at least 020
Insert size: 140000; agarose-fp
Insert size: 143263; sum-of-contigs
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                                                                              4614 4713: gap of 100 bp 1 length 6264 6363: contig of 1550 bp in length 6264 6363: gap of 100 bp 6364 9200: contig of 2837 bp in length 9201 9300: gap of 100 bp 9301 12704: contig of 3404 bp in length 12705 12804: gap of 100 bp 15804: gap 
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731 2440: contig of 1710 bp in length
2441 2540: gap of 100 bp
2541 4613: contig of 2073 bp in length
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contig of 4006 bp in length
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                                                                                                                                                                                                                                      Score 689.8;
Pred. No. 5.9;
0; Mismatches
                                                                                                                                                                                                                                      .8; DB 2;
5.9e-132;
ches 22;
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Gaps

COMMENT JOURNAL TITLE

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                                                           AUTHORS
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                                                                                                                                                                                                                                                                   67535 bp
Mus musculus clone RP24-506B15,
AC122733
AC122733.1 GI:21206317
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastlen,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarate,J., Campopiano,A., Chang,J., Chizaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
                                                                                              Unpublished
                                                                                                                 Birren,B., Linton,L., Nusbaum,C. and Lander,E. Mus musculus, clone RP24-506B15
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                          (bases 1 to 67535)
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Johnson, R., Jones, C., Kamat, A., Karattas, A., Kells, C., Larcoque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonalid, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schauer, S., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vessillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vonan, G., Talamas, J., Tesfaye, S., Vonan, G., Talamas, J., Tesfaye, S., Testaye, S., Testaye, S., Testaye, S., Testaye, S., Vonan, G., Talamas, J., Tesfaye, S., Vonan, G., Talamas, J., Tesfaye, S., Vonan, G., Talamas, J., Tesfaye, S., Vonan, G., Testaye, S., Vonan, G Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Direct Submission Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

COMMENT JOURNAL Submitted (25-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html

-- Genome Center

Contact: sequence_submissions@genome.wi.mit.edu Web site: http://www-seq.wi.mit.edu Center code: WIBR Center: Whitehead Institute/ MIT Center for Genome Research

Center project name: L17506 Center clone name: 506_B_15 Project Information

NOTE: This record contains 84 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be generich and allows overlap relationships among clones to be deduced be preserved. the record will be sequenced to completion. However, it should not be assumed that this clone is updated, the accession number will In the event that

9480 9580 10302 10402 11116 11116 1486: contig of 717 bp in length
1487 1586: gap of 100 bp
1587 2304: contig of 718 bp in length
2305 2404: gap of 100 bp
2405 3104: contig of 718 bp in length
1105 3204 8669 8769 4673 4773 7865: contig of 705 bp 10401: gap of 100 bp 11115: contig of 714 bp in length 11215: gap of 100 bp 11878: contig of 663 bp in length 9579: gap of 100 bp 10301: contig of 722 bp 8768: 5550: gap of 6248: cor 4772: gap of 5450: cor 3970: gap of 4672: cor 100 bp 200 bp 100 bp 10 1: gap of 100 bp 3870: contig of 666 bp in 669: contig of 669 bp in length 865: contig of 712 bp in length of 100 bp contig of 678 bp in of 100 bp contig of 702 bp contig of 100 bp of 711 bp in 100 bp of 698 bp in in length 'n ij length length length length

14307 14406: 13496 13595:

06: gap of 100 bp 15103: contig of 697 bp in length

5104 15203:

03: gap of 100 bp 15921: contig of 718 b

17520 17619:

16796:

16696: contig of 675 bp in length 798: gap of 100 bp 17519: contig of 723 bp in length 619: gap of 100 bp 18337: contig of 718 bp in length

ap of 100 bp:

18437:

9133 19232:

37: gap of 100 bp 19132: contig of 695 bp 32: gap of 100 bp

bp in length bp in length

19906: contig of 674 bp in length 20006: gap of 100 bp 20705: contig of 699 bp in length 20805: gap of 100 bp

15922 16021

gap of

100 bp

bp in length

1/8: gap of 12686: con

contig of 708 bp in length

12687 12786:

100 bp 10 length 595; gap of 100 bp 10 length 14306; contin ~ = 100 bp

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                                                                                                                         ACCCGCGCGCGACGCCTCGGTGCAGTGTTCACTCGGGCGCCGCACGCTGCAGCCTGCAG 18763
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47367 47466: gap of 100 bp
47467 47466: gap of 100 bp
47467 47466: gap of 100 bp
47467 47466: gap of 100 bp
48180 48279: gap of 100 bp
48280 48944: contig of 665 bp in length
48945 49044: gap of 100 bp
49045 49763: contig of 710 bp in length
49764 49863: gap of 100 bp
50571 50670: gap of 100 bp
50671 51393: contig of 722 bp in length
51393 51492: gap of 100 bp
51493 52104: contig of 692 bp in length
51493 52104: contig of 692 bp in length
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47367 47466: gap of
47467 48179: cont
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44238 44946; contig of 709 bp
44947 45046; gap of 100 bp
45047 45758; contig of 712 bp
45759 45858; gap of 100 bp
45759 45858; contig of 695 bp
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54696 ___55404: contig of
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41683 41782: gap of 100 bp
41783 42490: contig of 708 b
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1;

40152:

39269: contig of 705 bp in length 39369: gap of 100 bp 40052: contig of 683 bp in length 40152: gap of 100 bp 40863: contig of 711 bp in length 10963: gap of 100 bp

37662 37761:

36857 36956: 36064 36163: 35258 35357: 34437 34536:

32943: gap of 100 bp 3614: contig of 671 bp in length 3714: gap of 100 bp 34436: contig of 722 bp in length 3436: contig of 722 bp in length 35257: contig of 721 bp in length 3537: gap of 100 bp 36053: contig of 706 bp in length 36163: gap of 100 bp 36856: contig of 693 bp in length 36956: gap of 100 bp 3761: contig of 705 bp in length 3761: contig of 705 bp in length 3761: gap of 100 bp 38464: contig of 703 bp in length 39464: contig of 703 bp in length 39464: gap of 100 bp 38464: contig of 703 bp in length 39464: gap of 100 bp 39464: gap of 100 bp 39464: contig of 703 bp in length 39464: gap of 100 bp 39464: contig of 703 bp in length 39464: gap of 100 bp 39464: gap of 1

30484

31189: contig of

706

bp in length

30384 30483:

29670:

b/U: gap of 100 bp an length

28758 28857:

28063:

27169: contig of 699 bp in length 17269: gap of 100 bp 27963: contig of 694 bp in length 18063: gap of 100 bp 28757: contig of 694 bp in length 28757: gap of 100 bp 28750: contig of 713 bp in length 29570: contig of 713 bp in length

26470: 27269:

26370: contig of 704 bp

bp in length

25666: 24848:

25566:

gap of 100 bp in length 100 bp in length

24748

21499 21598: 20706 20805:

21498:

gap of 100 l

100 bp

bp in length bp in length

99 2302: contig of 704 bp
03 22402: gap of 100 bp
03 23108: contig of 706 bp
09 23208: gap of 100 bp
09 23208: gap of 719 bp
23 2407: gap of 100 bp

bp in length bp in length

31190 31289:

32844 32943: 32019 32118:

289: gap of 100 bp 32018: contig of 729 bp in length 118: gap of 100 bp 3843: contig of 725 bp in length 943: gap of 100 bp 3364: contig of 671 bp in length

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cleveland, C. D., Cox.C., Coyle, M.D., Dathorne, S.R., David, R., Cleveland, C.D., Cox.C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Ding, Y., Dinh, H.H., Davila, M.L., Ding, Y., Dinh, H.H., Davila, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Falls, T., Ferraguto, D., Edwards, C.C., Largis, A., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Herris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Herris, C., House, A., Hernandez, J., Herris, C., Hawis, A., Hernandez, J., Homs, J., Jackson, E., Hamilton, K., Johnson, R., Jolivet, S., Joudah, S., Kartovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Lozado, R.J., Lucier, A., Lucier, R., Luna, R., Ma, J., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Meil, G., Metzket, M., Moser, M., Meil, G., Metzket, M., Moser, M., Maleshwari, M., Mapua, P., Michell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Malla, D., Newtson, J., Newtson, N., Nguven, A., Ng
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Nikerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubkan,J., Rolie,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Schergten,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usman,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Ward,Moore,S., Warren,R., Washington,C., Wattington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Chen,R., Chen,Z., Chavazos,S.R., Chacko,J., Chavez,D., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Chen,R., Chen,Z., Chavazos,S.R., Chacko,J., Chavez,D., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Chen,R., Chen,Z., Chavazos,S.R., Chacko,J., Christopoulos,C., Chen,Z., Chen,Z., Chavazos,S.R., Chacko,J., Christopoulos,C., Chen,Z., Chen,Z., Chavazos,S.R., Chacko,J., Chavazos,D., Chavazos,C., Chen,Z., Chen,Z., Chavazos,S.R., Chacko,J., Chavazos,D., Chavazos,C., Chen,Z., Chen,Z., Chavazos,S.R., Chacko,J., Chavazos,D., Chavazos,C., Chen,Z., Chavazos,S.R., Chacko,J., Chavazos,D., Chavazos,C., Chen,Z., Chavazos,C., Chavazos,C., Chen,Z., Chavazos,C., Chavazos,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173007 bp DNA linear HTG 23-JUL-2002 Rattus norvegicus clone CH230-74L11, *** SEQUENCING IN PROGRESS ***, 59 unordered pieces.
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AC125993.1 GI:21671835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus.
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Submitted (02-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank.draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 59 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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138246
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138245:
143564:
143664:
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gap of unknown length
contig of 5319 bp in length
gap of unknown length
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Pred. No. 1.3e-116;
                                 89551 bp
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                                 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91;
                         SEQUENCING
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538

104554

478

418

104494

298

239

104314

104194

104374

23985 25117 25117 271218 271228 27128 27128 27128 27128 27128 27125 34225 34225 3712

75416 75516 78192 78192 78192 78192 882096 86303 86403 86403 86403 89945 90045 94438 9945 94438 94538 94538 1010895 1010895 10108195 10108195 1110808 1112008 1112008 111333 11133 11

linear

IN PROGRESS ***,

778

104791

104731 658 104674 598 104614

104851

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REFERENCE
AUTHORS
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bouck, J., Boule, S., Brieva, M., Brown, E., Bryant, N., P.,
Bouck, J., Bowle, S., Brieva, M., Brown, E., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T. F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chan, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Davila, M.L., Davy-Carroll, L., Dederich, D.A.,
Davila, M.L., Dalgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gabisi, A., Gao, J., Garcia, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Karlsson, E., Kelly, S., Khan, U., Lieu, F., Luca, R., Ma, J.,
Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martinez, E.,
Maheshwari, M., Mapua, P., Martin, R., Martinez, E.,
Mansey, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Martin, R., Martindale, A., Martinez, E.,
Massey, E., McLeod, M., Mohabbat, K., Morga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, L., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Sott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, T., Telfrod, B., Thomas, N., Thomas, N., Thomas, N., Thomas, S., Ward, Moore, S., Warren, R., Washington, C., Watliamson, A., Williamson, A., Williamson, A., Wilczyk, R., Wooden, S., Worley, K., Wu, Y., F., Zhou, J., Zorrilla, S., Neison, D., Weinstock, G., and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (31-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 89551)
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
                                                                                                                                                                                     Center project name: KAMV Center clone name: CH230-
                                                                                                                                                                                                                                                                           Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                ----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Center
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                                                                                                                                                                                              CH230-69F8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Allen,C.,
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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 48 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * runs of N, but th
* This record will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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Consensus quality:
Consensus quality:
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10742
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46367 bases at least Q30
48722 bases at least Q20
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FEATURES
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Best Local
                                                                                                                                                                                                                                                                  Matches 664;
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                                                                                                                                                                                   39627
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                                                                                                                                                                                                                                   49 CACCCCTGCCCGCATCCTTATCCGC----AGGCCACCAAAGCCGGGGGATGGCTGGAGGTTC 105
                                                                                                                                                                                                                                                                          Local Similarity 87.6%;
TCCTGGCAGACCGTAGCCCCGTTCTCGTCCGTGACCTTCTGTGGCCTCTCCTCCTCACTG
                              GACGCCGGATCGGGTTCCTGTCAACCCCGTGGCCACGCCGGCGCCGGGAGATCCCCCCGCGA 405
                                                                       CACCCATGCCCGCATCCTTACCCGCCCTCTGCAGCCAAAGCCGGGGATGGCTGGAGGTTT 39628
                                                           TCGGTGCAGTGTTCGCTCGGGCGCCCCCACACTGCAGCCTGGACGGCGCGCCGAGCCCCC
                                                                                                                                         GCCGCGGAGTACTTTGACAGCTATCAGCGAGCGCAGCTCATGGCCTTGCTGTCGCGAATG
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                                                                                                                                                                                 Conservative
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RCE 1 (bases 1 to 169908)

RS MUZDY, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barboria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burkett, C., Burch, K.L., Byrd, N.C., C., Carter, M., Carter, M., Carazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Ding, Y., Dinh, H.H., Duthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Enlay, T., Ferraguto, D., Flagg, M., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorfell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Hartis, C., Harris, K., Hartim, Havlak, P., Hawes, A., Hernandez, J., Howard, S., Hume, J., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kureshi, A., Landry, N., Leal, B., Levis, L.C., Lewis, L., Louise, C., Liu, W., Louiseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Machiner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Mansey, D., Pickens, R., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Payton, B., Pery, J., Perez, L., Peters, L., Pickens, R., Payton, B., Pery, J., Perez, L., Peters, L., R., Lender, R., Lucier, R., Lucies, M., Ren, Y., Roters, L., Payton, B., Pery, J., Perez, L., Peters, L., Payton, B., Pery, J., Perez, L., Payton, B., Pery, L., Roters, L., Payton, B., Pery, 
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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us norvegicus clone CH230-159N5, *** SEQUENCING IN PROGRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (06-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Gembank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 60 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N_{\star} but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.  \label{eq:constraint} % \begin{center} \begin{centen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
-----Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                       10435 TGCCTCTAGAGACCGGGCCTCCCCACAGAGCACTGAGCAGGACAAGGAGCGCCTGCGTTT 10376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10671 -GGAGAGGGGAGCCGGCACCCACCCGGGGACCCGGGAACCCGGGAGAGGTGGCAGT 10613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10731 GACCTTCGGTGGCCTCCTCCTCGCTGGAGGTTGCGGGGGACAGGCAGACGCCCACGAA 10672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10911 GGTGCAGGTGAACCCGCGCGCGCGATGCCTCGGTGCAGTGTTCGCTCGGGCGCGCACACT 10852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10791
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                                                                                                                                                                                                                                                                                                                                                                                             798 CCAGTT 803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGGTGGGAGCAGCCACCACCGGAGGACCGGAACAGTGTGGCGGCGATGCAGTCTGA 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCCCCTCGAGACCAGGCCTCCCCGCAAAGCACGGAGCAGGACAAGGAGCGCCTGCGTTT 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCCGGGAGTGAGGAGCCACCTCCTGCTGTCGAGATGGCTCAGGACCCCAGTGACGTGGC 10436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TG---GGCAGGAGCAGCCACCGCGGGAGGACCCGGACAGTGTGGCGGCGATGCAGTCTGA 10496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGGAGGGCGATGTTCAGGCTGCAGGGCAGGC 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGAGAGGGGAGCCCGGCATCCTCGGGGACCCGGGAACCGGAGCCGAGAGAGGTGGCCGC 557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCTCATGGCCCTGCTGTCGCGGATGGGTCCCCGGTCG-GTCAGCAGCCGTGACGCTGC 257
                                                                                                                                                                                                  AC108848 212848 bp
Mus musculus clone RP23-300K5, v
            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                               Mus musculus
                                                                                 Mus musculus.
                                                                                                       HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                               AC108848.2 GI:20336129
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113734: contig of 4248 bp in le
113834: gap of unknown length
116884: contig of 3050 bp in le
116894: gap of unknown length
121008: contig of 4024 bp in le
121108: gap of unknown length
124634: contig of 5573 bp in le
124734: gap of unknown length
130307: contig of 5573 bp in le
130307: gap of unknown length
130407: gap of unknown length
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Pred. No. 4.9e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                    P DNA 1:
WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 169908;
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AUTHORS
TITLE
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Sequencing vector: Plasmid; n/a; 100% of reads Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 200069 bases at least Q40
                                                                                                                        Center project name: L21014 Center clone name: 300_K_5
                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
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RS Birren, B. Linton, L. Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Cohang, J., Cohangelo, M., Collins, S., Collymore, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Dlaz, J.S., Dodge, S., Faro, S., Ferreira, P., Filtzhugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Milenga, V., Murphy, T., Maylor, J., Wuyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Petterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Riaback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Sahron, J., Zembek, L., Zimmer, A. and Zody, M.
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Submitted (28-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 28, 2002 this sequence version replaced gi:18450109. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Alien, N., Anderson, S., Barna, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Dlaz, J.S., Dodge, S., Faro, S., Conse, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birren,B., Linton,L., Nusbaum,C. and Lander,E. Mus musculus, clone RP23-300K5
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the accession number will be preserved.

1 641: contig of 641 bp in length
642 741: gap of 100 bp
742 1427: contig of 686 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 36 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces \frac{1}{2}
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Quality coverage: 5.7 in Q20 bases; sum-of-contigs
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82724 8787
87876 87975:
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77031
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67332 709
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24824 27746: contig of 2923 bp in length
27747 27846: gap of 100 bp
27847 29873: contig of 2027 bp in length
29874 29973: gap of 100 bp
29874 33212: contig of 3239 bp in length
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20008 21470: contig of 1463 k
21471 21570: gap of 100 bp
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                                                                                                                                                                                                                                        77030: gap of 100 bp 10 length 82623: contig of 5593 bp in length 82723: gap of 100 bp 10 length 87875: contig of 5152 bp in length 87875: gap of 100 bp 100
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104305: gap of 100 bp
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119104: contig of 14799 bp in length
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15335: cont
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63792: contig of 1960 bp in length
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67231: contig of 3339 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       756 CTCCCCGCAAAGCACGGAGCAGGAGCAGGAGCGCCTGCGTTTCCCAGTT 803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RS Birren, B. Linton, L. Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Camarata, J., Campoplano, A., Chang, J., Chazaro, B., Choepel, Y., Colangel, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Goldes, S., God, S., Goyette, M., Graham, L., Grand-Pierre, N., Gande, S., God, S., Goyette, M., Graham, L., Grand-Pierre, N., Ganders, G., Gardyna, S., Kanata, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., McCarthy, M., Marquis, N., Matthews, C., McCarthy, M., MacMan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Milonga, V., Murphy, T., Naylor, J., Mquyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Connell, P., O'Neil, D., O'lver, J., Meterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Schauer, S., Schupback, R., Seaman, S., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Tasvis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zahnoun, J., Zembek, L., Zimmer, A. and Zody, M.
              TRESCARCIO, 320 Charles Street, Cambridge, MA 02141, USA

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Barren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chargaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lianazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacCarthy, M., McEwan, P., McKernan, K., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Milova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Travis, N., Trigilo, J., Vassiliev, H., Volan, B., Mulx, Wyman, D., Ye, W.T., Young, G., Ville, R., Volan, R., Wilson, B., Wu, X., Wyman, D., Ye, W.T., Young, G.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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1 (bages 1 to 212848)
Birren, B. Linton, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (31-JAN-2002) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
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17770 199
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Submitsed (28-APR-2002) Whitehead Institute/MIT Center for Genome Submitsed (28-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320-Charles Street, Cambridge, MA 02141, USA On Apr 28, 2002 this sequence version replaced gi:18450109. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * 8976 9075; gap of 100 bp 10258 11357; gap of 100 bp 10258 10357; gap of 100 bp 10358 11609; contig of 1182 bp in length 10358 11609; contig of 1251 bp in length 11609 11708; gap of 105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 36 contigs. Gaps hetween the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes to the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 641: contig of 641 bp in length
642 741: gap of 100 bp
1428 1527: gap of 100 bp
1528 3170: contig of 1643 bp in length
1528 3170: contig of 1643 bp in length
1739 3171 3270: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 200069 bases at least Q40 Consensus quality: 206302 bases at least Q30. Consensus quality: 206218 bases at least Q30 Consensus quality: 208218 bases at least Q30 Insert size: 209346; sum-of-contigs Quality coverage: 5.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: L21014 Center clone name: 300_K_5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------ Genome Center Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3271 4396: contig of 1126 bp in length
4397 4496: gap of 100 bp
4497 5909: contig of 1413 bp in length
                                                                                                                                                                                                                      21470: ^^
                                                                                                                                                                                                                                                                     19907:
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1083: contig of 1574 bp in length

13: gap of 100 bp

8975: contig of
                                                                                                                                                                   007: gap of 100 bp
21470: contig of 1463 bp in length
570: gap of 100 bp
23086: contig of 1516 bp in length
                                                                                                                                                                                                                                                                                                                                                                                   708: gap of 100 bp 13289: contig of 1581 bp in length 189: gap of 100 bp 15335: contig of 1946 bp in length 185: gap of 100 bp 16250: contig of 815 bp in length
                                                                                                                86: gap of 100 bp
24723: contig of 1537 bp in
                                                                                                                                                                                                                                                                                                                                   17669: contig of 1319 bp in length
                                                                   27746
16: gap of 100 bp
29873: contig of 2027
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                                                                                          gap of
                                                                                                                                                                                                                                                                           p of 100 bp
contig of 2138 bp in length
                                                             contig of 2923 bp in length
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                                 100 bp
                                                                                          100 bp
        bp in length
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FEATURES
                                                             Matches
88270 GGCGGGCGAGGCGCGGAACGCACCCATGTTCCCCGGCGAGCACGTTCCACCCCTGCCCGCA 88211
                                                                                                                                             misc_feature
                                                                                                                                                                             misc_feature
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                                                                            Local
               3 GGCGGGCGAGGCGCGGGACCCATGTTCCCGGCGAGCACGTTCCACCCCTGCCCGCA 62
                                                                310;
                                                                                Similarity
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149071 165714
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165815 18336
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132400 14897
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                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment" 3271. .4396
                                                                                                                                                                                                                                                                                                            /note="assembly_fragment"
9076. .10257
                                                                                                                                                                                                                                                                                                                                            7684
                                                                                                                                                                                                                                                                                                                                                                           6010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment"
1528. .3170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-300K5"
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11709. .13289
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16351. .17669
                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment"
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                                                                                                                              /note="assembly_fragment"
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13390. .15335
                                                                                                                                                                                                                                                                                         /note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82723: gap of 100 bp
87875: contig of 5152 bp in length
87975: gap of 100 bp
93774: contig of 5799 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67331: gap of 100 bp
70922: contig of 3591 bp in
71022: gap of 100 bp
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104205: contig of 10331 bp in length
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v: gap of
165714: C
1817
                                                                            23.5%;
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210291: contig of 26822 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5814: gap of 100 bp
183369: contig of 17555 bp in
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312: gap of 100 bp
61732: contig of 20420 bp in length
332: gap of 100 bp
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82623: contig of 5593 bp in
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92: contig of 1960 bp in length
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contig of 3339 bp in length
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contig of 16644 bp in
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contig of 16571 bp in length
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                                                                              Score 299.8; DB 2; Pred. No. 1.4e-51;
                                                                Mismatches 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88210 TCCTTATCCGCAGGCCAACCAAAGCCGGGGATGGCTGGAGGTTCGGAGCCAGGGGGCTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88030 CAGCCGTGACGCTGCGGTGCAGGTGAACCCGCGCGCGACGCCTCGGTGCAGTGTNNNNN 87971
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                       Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Erantz, P., Frantz, P., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Harris, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Joudah, S., Jackson, L. E., Jackson, E., Kelly, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. E., Jackson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L. Li, J., Li, W., Loulseged, H., Li, J., Li, X., Lucker, A., Lucier, R., Luna, R., Ma, J., Lu, Y., Lucker, R., Luna, R., Ma, J., Lu, Y., Lu, Y., Lucker, R., Luna, R., Ma, J., Lu, Y., Lucker, R., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Morris, S., Moser, N., Nauven, N., Newtson, N., Nguyen, N., Nguyen, N., Nguyen, N., Naukenson, E., Nwokenkwo, S., Oouh, M., Okwunoni, G., Naukenson, E., Nwokenkwo, S., Oouh, M., Okwunoni, G., Sanda, M., Sanda, N., Naukenson, E., Nwokenkwo, S., Oouh, M., Naukenson, R., Naukenson, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus clone CH230-69F8, 48 unordered pieces. AC127083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Norway rat
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Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M.,
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, *** SEQUENCING IN PROGRESS
                 Okwuonu, G.
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Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolie, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (31-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 48 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 42659 bases at least Q40
Consensus quality: 46367 bases at least Q30
Consensus quality: 48722 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Baylor College of Medicine Center code: BCM
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        1152
2323
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                                                                                                                            Direct Submission Submitted (08-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                        Direct Submission
Submitted (03-JUL-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
           Direct Submission
Submitted (30-SEP-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Sep 8, 1999 this sequence version replaced gi:5630058.
                                                                                                                                                                                             Waterston, R.H.
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Unpublished
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING

INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RCCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P. Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8, The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
VECTOR: pbACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-349G4. Actual end of this clone is at base position 138890 of RP11-485G2.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1011 GCCACGTGGACCCTAAACGCCCCCCATCGGCAAGACTTGTGTGGGAGATGCAAGGACAAAC 1070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity les 202; Conserv
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Garad, Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Grand, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Kenatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Looke, K., Madonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Menga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCTATCCTGTGTGAGCACTTTCAGCTTCAAATA 28387
                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 151961)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 2, clone RP11-77F17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome 2 clone RP11-77F17 map SEQUENCE, 10 unordered pieces.
                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC037443.2 GI:7960458
                                                                                                                                                                                                                                                                                                             (bases 1 to 151961)
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39477
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41875. .42095
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40713. .40816
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40301. .4033
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39061. .39116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="MER4-group" 38558. .38976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="match to EST AL046241 (NID:95434325)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="(TC)n"
10405. .40690
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73.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _tamily="(TAAA)n"
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REFERENCE

TITLE JOURNAL

AUTHORS

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Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, T., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Rogov, P., Rothman, D., Rogov, P., Rogo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                     be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                  as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 151961)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 194000; agarose-fp
Insert size: 151061; sum-of-contigs
Quality coverage: 4.5 in Q20 bases; agarose-fp
Quality coverage: 5.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: M13; M7815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 147226 bases at least Q40 Consensus quality: 149421 bases at least Q30 Consensus quality: 150378 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: L9226
Center clone name: 77_F_17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                            1452 1551: gap of 100 bp
1552 3695: contig of 2144 bp in length
3696 3795: gap of
3796 6752: contig
6753 6852: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- Summary Statistics
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                                                                      100 bp
of 2957 bp in length
                   100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                  41665 CTGCAAGGACTGTGACATCCAATGGGAGGGTGCTTATGTGTGGTGTGTATAGAGACCTAA 41606
41428 ACCTATCCTGTGTGAGCACTTTCAGCTTCAAATA 41395
                                                                                                                                                                                                                                   41605 TAAGAACTACTTCAA---AGTTTTACAGAACTTGTCAGAAGTCTTATAACTCGTACCAAG 41549
                                                                            41488 TCTACATAGACCCTAAACGGCCCTATTGTCAAGATTTGTGTGGGAGATGCAAAGGCAAAC 41429
                                   1071 GCCTGTCCTGCGACAGCACCTTCAGCTTCAAATA 1104
                                                                                                               1011 GCCACGTGGACCCTAAACGCCCCCCATCGGCAAGACTTGTGTGGGAGATGCAAGGACAAAC 1070
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                                                                                                                                                                                              891 TAAGGTGTTACTTCAAACAGTTCTGCCGAGTGTGTGAGAAATCCTACAACCCTTACAGAG 950
                                                                                                                                                                                                                                                                                                                                                         GGGAAGATAACAGCAATCAAAGTTGTAAATAAACTAGATGTTGCTGGCTAGCAAGATTTC 41489
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105704 105803:
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18027 18126: gap of 100 bp
18127 30673: contig of 12547 bp in length
30674 30773: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105804..151961
/note="assembly_fragment"
a 28505 c 28546 g 46219
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3796. .6752
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45042. .58179
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30774. .44941
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source
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Consensus quality: 199700 bases at least 040
Consensus quality: 201820 bases at least Q30
Consensus quality: 203416 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: M13; 45%
Sequencing vector: plasmid; 55%
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On Oct 18, 2001 this sequence version replaced gi:14523031.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (22-JUN-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site:http://genome.wustl.edu/gsc/index.shtml
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Waterston, R.H.
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                            58458: contig of 46009 bp in length 58558: gap of unknown length 204268: contig of 145710 bp in length
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1221: gap of unknown length
2388: contig of 1167 bp in length
2488: gap of unknown length
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Matches 202; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 187578)
Sulston, J. E. and Waterston, R.
Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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Homo sapiens BAC clone RP11-191J2 from 4,
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Data from AC032000 and AC024191 were used to finish

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5 (bases
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Direct Submission
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Wang,C., Meyer,R. and Dignan,G.
The sequence of Homo sapiens BAC clone RP11-191J2
Unpublished (2001)
3 (bases 1 to 187578)
NEIGHBORING SEQUENCE INFORMATION: The clone sequenced to the left is RP11-473N2; the clone sequenced to the right is RP11-757K22, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-191J2; actual end is at base position 17325 of RP11-757K22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (20-APR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6. on Apr 5, 2002 this sequence version replaced gi:19807902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston, R
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                                                                                                                                                                                                                                                                                   The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                       and coworkers at http://www.chori.org
                                                                                                                                                                                                                                 Research Genetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0191J02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://genome.wustl.edu/gsc
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                                                                                                                                                                                                                                    Genomics 51:1-8. The clone may be obtained either from enetics, Inc. (http://www.resgen.com) or Pieter de Jong
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Polymorphisms have been identified between AC032000, AC024191, and

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11491. .1
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4161. .4181
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12830
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10662. .10970
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4557. .4577
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4178. .4188
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10536. .11223
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1017. .1100
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/chromosome="4"
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/note="similar to Homo sapiens EST AI265985 (NID:g3884143)
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(NID:g10149129)"
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14447. .14813
                                                                                                                /note="similar to Mus musculus EST BI407638 (NID: g15168561)"
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                                                                                                                                                                                           TGACAGACAGTGTTACTTGGATATAAAGCCTGTGAATAAAAGGTATTGCAA 1257
                                                                                                                                                                                                                                                                            TAATGGAATGGACAAGTGAGCTTTCTCCCCTCTTCACCTCTTCCCTTTCCAAATTCTTCA 1206
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/note="similar to Homo sapiens EST BG034944
(NID:g12428670)"
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14878. .15146
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14873. .14900
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au43f12.x1"
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/note="similar to Homo sapiens EST BF695420
(NII:911980828)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="match to EST BG995513 (NID:g14399583)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14477. .14827
/note="similar to Homo sapiens EST AA143121 (NID:g1712509)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"similar to Mus musculus EST BE848577
(NID:g10306847) uw38h07.y1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to Homo sapiens EST BE378224
(NID:g9323589)"
                  GI:15879714
                                                                genomic sequence surrounding NotI site,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          te="similar to EST BQ021037 (NID:g19756307)"
23. .14827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.5%;
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Pred. No. 1.5e-17;
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 TCGGGCGCCGCACGCTGCAGC 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   528 TCTTTCCCGGGTGCGGGCGTCTGACGGCCGAGTA-TTTGACAGCTACCAGCGGGAGC 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAGCCGTGACGCTGCGGTGCAGGTGAACCCGCGCGCGACGCCTCGGTGCAGTGTTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGCTGCGACGTGNCGGTGCAGGTGAGCCCGCGCATCGACGCCGCGGTACAGTGCTCGC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCTCATGGCTCTCCTGGCGCAGGTGGGGCCGGGTCTCGGACCGCGCGCCCGCAGGTCCG 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138;
                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 125020)

Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang, H.S., Ingersoll-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A., Potter, N.T., Ross, C.A. and Margolis, R.L.

A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2

Nat. Genet. 29 (4), 377-378 (2001)
                        2 (bases 1 to 125020)
Holmes,S.E., Ingersoll-Ashworth,R.G., Ross,C.A. and Margolls,R.L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                     125020 bp DNA linear I
Homo sapiens junctophilin 3 (JPH3) gene, partial cds
AF429315
Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical
                                                                                                        21583737
                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                       AF429315.1 GI:17646244
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Submitted (16-MAY-2001) Microbiology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 694)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sweden
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zabarovsky, E.R
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/db_xref="taxon:9606"
/clone="NR5-ID16C"
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Pred. No. 7.1e-05;
0; Mismatches 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17723 KSYMMCYCYMYRMSSYMSYYYKCYSCMGMSSTSYSYSCCWKMSSWGSCYKCMKYYSGWSS 17664
                                               17303 SMKKMKRSSWSKCYSTKSYKSGRRKSKGWGRSTKSKAKSSMRMAGSKCTYGSSYWSNNRR 17244
                                                                                                                                             17363 MRGSMSSKGWRGYAGRGCYSSSMWSTRKRRSKCYSYKSYKKGRGKMKGWGGMKRGSKYWS 17304
                                                                                                                                                                                                                                           17423 CCMKKKGCTGYRGMSSKKSGYKSMRGMRGSSYSTSCWKSCWGYSWMKCMKYMSYKKKRRS 17364
                                                                                                                                                                                                                                                                                                                                      17483 GSYGSTGRSMKKKKGYSKYSRGMKGKKKTCYCMWKYYKYRKTSMCWWYYMKSWGYKRYKR 17424
                                                                                                                                                                                                                                                                                                                                                                                                                                    17543 CMMRSSKSSWSMSMARSSWCMGWGAGYRRSKRSAGWGAGWRSSKGKRSTGMKRACSKKT 17484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17603 SYWKCCAKWWMSYCCWSYCMTYYYSKSCTYKSSTCYKRGGYYWGSKTCYSAGGKSRSMYY 17544
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                                                                                           480 CAGGCAGACACCCACGAAGGGAGAGGGGAGCCCGGCATCCTCGGGGAACCCGGGAACCGGA 539
                                                                                                                                                                                            420 AGCCCCGTTCTCGTCCGTGACCTTCTGTGGCCTCTCCTCCTCACTGGAGGTTGCGGGAGG 479
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  540 GCCG&GAGAGGTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGAGGGCGATGT 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAGCCGTGACGCTGCGGTGCAG-GTGAACCCGCGCGCGACGCCTCGGTGCAGTGTTCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSTSMGYYSSTSCKKYKCSWSSMYKCKTSKSYRRKRSYYYWGGGKRAKKKYYCAGRRRRM 17604
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                                                                                                                                                                                                                                                                                       TCCTGTCAACCCCGTGGCCACGCCGGCGCGCGGAGATCCCCGCG-ATCCTGGCAGACCGT 419
                                                                                                                                                                                                                                                                                                                                                                                        CTCGGGCGCCGCACGCTGCAGCCTGCAGGGTGCCGAGCCCAGCCCCGACGCCCGATCGGGT 360
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/note="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
complement(35581. .35746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="junctophilin 3"
/protein_id="AAL40941.1"
/protein_id="AAL40941.1"
/db_xref="G1:17646245"
/translation="MSSGGREWFDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWS
/translation="MSSGGREWFDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(<36507. .>36887)
/gene="JPH3"
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/db_xref="taxon:9606"
/chromosome="16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGAKYEGTWSNGLQDGYGTETYSDG"
32731 c 30696 g 28283 t
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                                                                                                                                                                                                                                                                                                                                  17123 GWGRKGRKCMSSRKMKMYKSYYRRKRWMTCMKMCYSMYMAMYCRSMCCMCMCKSCCGCYS 17064
                                                                                                                                                                                                                                                                                                                                                                                                                                                 17183 CYKGRMSSKSCYRSGTRRRCMKSKCRRGSRGKSMGMTRGRSGGKTSYSAKGSGRGCYYCW 17124
16943 CWSSCWWSSMRKKSKGGSWAKGMVWDKGSVSTDKSDKMBSRSBSKVKSKWSMSRRGKYYY 16884
                                                                                                              17003 YKGGGSWGGKGGKSTRGSSAGKKSSYKKMSCCARYKSMSYSKCYSRWMWCMSYYYCWGGK 16944
                                                                                                                                                                                                                            17063 MGMSSYSYSGKYSWGMKSYMWRSYYSKRSTSKAWRSSKRGMGTGGRYKGGGRSYGKGGGS 17004
                                                                                                                                                                                                                                                                                                                                                                                       660 GGCGGCGATGCAGTCTGAGCCTGGGAGCGAGGAGCCATGTCCTGCCGCAGAGATGGCTCA 719
                                                                                                                                                               CAAGGAGCGCCTGCGTTTCCAGTTCTTAGAGCAGAAGTACGGCTACTATCACTGCAAGGA 839
                                                                                                                                                                                                                                                                           GGACCCCGGTGATTCGGATGCCCCTCGAGACCAGGCCTCCCCGCAAAGCACGGAGCAGGA 779
                                                    TCAGGCTGCAGGGCAGGCCGGTGGGAGCAGCAGCCACCGGAGGACCGGAACAGTGT
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Search completed: January 19, 2003, 22:13:21 Job time : 5277 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                  /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
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                  US-08-311-363-12
US-08-232-463-14
US-08-455-2008-11
US-09-075-556-179
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US-09-075-5543A-8
US-08-193-078B-8
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US-08-949-386-8
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12, Appl
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179, App
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Sequence 21, Appl	21	21	21	163	159	163.	163	163	163	163	51.		163,	163			Sequence 163, App

ALIGNMENTS

RESULT 1 US-07-745-206A-12

Sequence 12, Application US/07745206A Patent No. 5429921

INFORMATION:

APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: McCue, Ann
APPLICANT: Feldman, Daniel
TITLE OF INVENTION: Human Cal
TITLE OF INVENTION: Methods

NUMBER OF SEQUENCES:

Human Calcium Channel Compositions Methods

and

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US-07-745-206A-12
                                                                                                                                                                                                                                                                                                                 TELEPHONE: 312-372-7842 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 5467 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                     FEATURE:
                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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NAME/KEY: CDS
LOCATION: join(144..3164, 3168..3245, 3249..3386, 3390
LOCATION: .3392, 3396..3488, 3495..3539, 3543..3581,
LOCATION: ..3587, 3591..3626, 3630..3689, 3693..3737,
LOCATION: ..3746, 3750..4823, 4827..4841, 4845..5006,
LOCATION: ..5096, 5100..5306, 5310..5366, 5370..5465)
                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: unl
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CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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EDNESS: unknown
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135 S. LaSalle
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3100
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REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
                                                                                                                FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Brenner, Robert TITLE OF INVENTION: Human CITITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3160 TGAGAT 3165
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 CTGTCAACCCCGTGGCCACGCCGGGGGGGGGAGATCCCGGGATCCTGGCAGACCGTAGC 422
                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      483
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                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                     NAME:
                                                                                                                                                      APPLICATION NUMBER: US 07/745,206
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                                                                                                 Seidman, Stephanie L
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                                                                                                                                                                                                                                                                                                                                                                                                 1660 Union Street
                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harpold, Michael
                : (619)238-0999
(619)238-0062
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Pred. No. 0.00048;
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08232463 Patent No. 5670367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 5467 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                             APPLICANT: DORNER, F.
APPLICANT: SCHELFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
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           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OFWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               543 GAGAGAGGTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCAAGCGAGGAGGGCGATGTTCA 602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                663 GGCGAT 668
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LOCATION:
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                                                                                                                                                  ZIP:
                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                         ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road,
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCTGCAGGGCAGGCCGGGTGGGAGCAGCAGCCACCACCGGAGGACCGGAACAGTGTGGC 662
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.3392, 3396..3488, 3495..3599, 3543..3581, 3585
.3587, 3591..3626, 3630..3689, 3693..3737, 3744
..3746, 3750..4823, 4827..4841, 4845..5006, 5010
..5096, 5100..5306, 5310..5366, 5370..5465)
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46.7%;

 Mismatches

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Pred. No. 0.00048;
                                                                                                                                                                                                                             Suite 500
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RESULT 4
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                                                                                                                                                                                                   Sequence 11, Application US/08456200B Patent No. 6229000
                                                                                         GENERAL INFORMATION: JURGEN; Weingartner, Bernhard;
APPLICANT: Franz, Jurgen; Weingartner, Bernhard;
APPLICANT: Unterbeck, Axel; Rae, Peter
TITLE OF INVENTION: TISSUE-SPECIFIC HUMAN NEURONAL
TITLE OF INVENTION: CALCIUM CHANNEL SUB-TYPES AND
TITLE OF INVENTION: THEIR USE
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STREET: 000
STRY: Tarrytown
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 14:
                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SPRUNG HORN KRAMER & WOODS
STREET: 660 White Plains Road
                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1208
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LENGTH: 7218 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           585 CGAGGAGGCGATGTTCAGGCTGCAGGGCAGGCCGGGTGGGAGCAGCAGCCACCACCGGA 644
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               899149
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US-08-456-200B-11
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MEDIUM TYPE: Diskette, 3
MEDIUM TYPE: Storage
COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 11:
1993 CACGAGGCTGTGGAGAAGGAGCCACNGAGAAGGAGGCCCACGGAGAAGGAGGCTGAGAT 20$1
                                                                                                                                                                                                                                                                                                                                                                                                                             1696 CGCA-GCCACAGCAAGGAGGCCGCGGGGCC--CCCGGAGGCGGGGGAGCAGCGGCCGGACCAGAGCAGCGCCGA 1762
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APPLICATION NUMBER: DE 41 10 785
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
                             610 GGGCAGGCCGGGTGGGAGCAGCAGCCACCACCGGGAGGACCGGAACAGTGTGGCGGCGAT 66
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APPLICATION NUMBER: 07/858,278
FILING DATE: 26-MAR-1992
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APPLICATION NUMBER: US/0
FILING DATE: 31-MAY-1995
                                                                                                                                                                                                             490 CCCACGAAGGGAGGGGGAGCCCGGCATCCTCGGGGACCCGGGAACCGGAGCCGAGAGAG 549
                                                                                                                                                                                                                                                                                                                                                                                370 CCCCGTGGCCACGCCGGCGCGCGAGATCCCGCGATCCTGGCAGACCGTAGCCCCGTTC 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 CGCACGCTGCAGGCTGCAGGCTGCCGAGCCAGCCCGACGCCCGATCGGGTTCCTGTCAA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 GACGCTGCGGTGCAGGTGAACCCGGGGCGCGCGACGCCTCGGTGCAGTGTTCACTCGGGCGC 30
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TOPOLOGY: Lir
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Local Similarity 48.0%;
les 201; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Kurt G. Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                          GGCGCCAAGGGCGAGCGGNGNGCGCGGCACCGCGGCGCCCCGAGCGGGGCCCCGGGAG 1932
                                                                                                                                                                                                                                                        GAGCGGGAGCCCCGACGCCACCGCGCACCGGCACCAGGATCCGAGCAAGGAGTGCGCC 1872
                                                                                                                                                                                                                                                                                                  GCCCCAGGCCCGAGGGCGGCGGCGGCACCACCACCGGCGCGCGCTCCCCGGAGGAGGCGGCC 1812
                                                                                    GCGGAGAGCGGGGAGCAGCCGGCGCGGCACCGGGCCCGGCACAAGGCGCAGCCTGCT 1992
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US-09-072;596-174
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Patent No. 6350456
Sequence 174, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT
NAME: Maki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                        179
                                                                                                                                                                                                                                                                                                      518 CCTCGGGGACCCGGGAACCGGAGCCGAGAGAGGTGGCCGCGAGGAAAGCGGTCCCCCAGC 577
                                                                                                                                                                                                                                                                                                                                                                                                         119 CTTCACCCAAGGCGCCGACGGCAACGCCGGCAACGGCGGTGACGGCGGGGTCGGCGGCAA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                      458 CCTCACTGGAGGTTGCGGGAGGCAGGCAGACACCCACGAAGGGAAGGGGAGGCCCGGCAT 517
                                                                                                                                                                    698 GTCCTGCCGCAGAGATGGCTCAGG 721
                                                                                                                                                                                                                                     638 CACCGGAGGACCGGAACAGTGTGGCGGCGATGCAGTCTGAGCCTGGGAGCGAGGAGCCAT 697
                                                                                                                                   359 CGGCGGCGACGGTGCACTCTCAGG 382
                                                                                                                                                                                                                                                                        COMPUTER: IBM. PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                        98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49.6; DB 4
Pred. No. 0.0021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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GENERAL INFORMATION:

APPLICANT:
APPLICANT:

Harpold, Michael Ellis, Steven

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US-09-072-596-174
; Sequence 8, Application US/08455543A; Patent No. 5792846
                                    US-08-455-543A-8
                                                     RESULT 7
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Best Local Similarity 49.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                      518 CCTCGGGGACCCGGGAACCGGAGCCGAGAGAGGGGGCGGCGAGGAAAGCGGTCCCCCAGC 577
                                                                                                                                                                                                                                                                                                                                                                                      119 CTTCACCCAAGGCGCGACGGCAACGCCGGCAACGGCGGTGACGGCGGGGTCGGCGAA 178
                                                                                                                                                                                                                                                                                                                                                                                                                         458 CCTCACTGGAGGTTGCGGGAGGCAGGCAGGACACCCACGAAGGGAAGAGGGGAGCCCGGCAT 517
                                                                                                                                                                                                            638 CACCGGAGGACCGGAACAGTGTGGCGGCGATGCAGTCTGAGCCTGGGAGCGAGGAGCCAT 697
                                                                                                                                                                                                                                                                                 578 CGCGAAGCGAGGGCGATGTTCAGGCTGCAGGGCAGGCCGGGTGGGAGCAGCAGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 05-MAY CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 6300 C
                                                                                                         359 CGGCGGCGACGGTGCACTCTCAGG 382
                                                                                                                                        698 GTCCTGCCGCAGAGATGGCTCAGG 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Maki, David J.
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                           130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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Lodes, Michael J.
Hendrickson, Ronald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Houghton, Raymond
Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEED and BERRY LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49.6; DB 4; Length (
Pred. No. 0.0021;
0; Mismatches 134; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 400;
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US-08-455-543A-8
                Query Match
 Best Local Similarity
                                                                                                                                                                                                                                                                                   TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: WO POSITION DATE: 04-APR-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/455,543A FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: APPLI 4, 1994
DBTOD NODITION NOMEN: 01944
                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 04-APR-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                              FEATURE:
                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                             LOCATION:
                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                         TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0 FILING DATE: 04-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 04-AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 0 FILING DATE: 30-NOV-1990
                                                                              NAME/KEY:
                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                            NAME/KEY:
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                                                                                                                                                                                                                                                                        LENGTH:
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                                                                OCATION:
                                                                                                                                                                                                                                                     nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                  Seidman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                California
                                                                                                                                                                                                                                                                    7175 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Brown, Martin, Haller & McClain
                                                                                                                                                                                                                                                                                                                   (619)238-0062
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1..143
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Feldman, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FastSEQ Version 1.5
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                                                                                                                                                                                                                           linear
                                                                                                                                                                            CDS
                                                                6855..7175
                                                                                                                                                          144..6857
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                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-FEB-1990
                                                                                                                                                                                                                                        double
                                                                                                                                                                                                                                                                                                                                                                                                 Stephanie L
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: 57
 3.8%;
48.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO PCT/US89/01408
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Score 49;
Pred. No.
DB 1;
0.0094;
             Length 7175;
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RESULT 8
US-08-193-078B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/868,354
FILING DATE: 10-APR-1992
PRIOR APPLICATION DATA:
                               FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seldman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 63
                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/193,078B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3048 GCGGAGAGCGGGAGGAGCCGGCGCGCGCGCACCGGGCCCGGCACAAGGCGCAGCCTGCT 3107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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CITY: S
STATE:
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                                                                                                                                                                                                               FILING DATE: 07-FEB-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 92101
                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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Feldman, Daniel
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Ellis, Steven
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                                                                                                                       US 07/745,206
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COMPUTER READABLE FORM:

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US-08-193-078B-8
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US-08-223-305C-8
                                                                                                                                                                                                                                                   Patent No. 5851824
GENERAL INFORMATION:
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                                                                       NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Ma
                                                                                                                                                                                                                                                                                                                                                                  2988
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                                                                                                                         APPLICANT: Brenner, Robert TITLE OF INVENTION: HUMAN C. TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2868 GGCCCAGGCCCGAGGGCGGCCGGCGCGCACCACCGGCGCGCGCGCTCCCCGGAGGAGGCGGCC 2927
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                COUNTRY:
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92101-2926
                            San Diego
California
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                                                             1660 Union Street
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                USA
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Pred. No. 0.0094;
                                                                             Haller & McClain
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US-08-223-305C-8 TELEFAX: (619)238-0062 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/745,206
PRIOR DATE: 15-AUG-1991 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION: CURRENT APPLICATION DATA: FILING DATE: 20-FEB-1990 PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: 2928 GAGCGGGAGCCCCGACGCCACCGCGCACCGGCACCAGGATCCGAGCAAGGAGTGCGCC 2967 2751 GAGGCCCCGAAGGCGGAGAGCGGGGAGCCCGGTGCCCGGGAGGAGCGGCCGCGGCGGCCGCAC 28110 TELECOMMUNICATION INFORMATION: PRIOR APPLICATION DATA: MOLECULE TYPE: 250 GACGCTGCGGTGCAGGTGAACCCGCGCGCGCGACGCCTCGGTGCAGTGTTCACTCGGGCGC 3 370 CCCCGTGGCCACGCCGGCGCGCGGAGATCCCCGCGATCCTGGCAGACCGTAGCCCCGTTC 310 CGCACGCTGCAGCCTGCAGGGTGCCGAGCCCAGCCCCGACGCCCGATCGGGTTCCTGTCAA 36 COMPUTER: IBM CO
OPERATING SYSTEM:
SOFTWARE: FastSE NAME/KEY: LOCATION: APPLICATION NUMBER: 07/868, FILING DATE: April 10, 1992 APPLICATION NUMBER: US/08/223,305C FILING DATE: April 4, 1994 REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52 FILING DATE: FILING DATE: FILING DATE: MEDIUM TYPE: TELEPHONE: APPLICATION NUMBER: WO POSTLING DATE: 04-APR-1989 APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: LOCATION: NAME/KEY: LOCATION: NAME/KEY: TOPOLOGY: STRANDEDNESS: GGCCCAGGCCCCGAGGGCGGCGCGCGCACCACCGGCGCGCTCCCCGGAGGAGGCGCCC CGCA-GCCACAGCAAGGAGGCCGCGGGGCC--CCCGGAGGCGCGGAGCGCGAGCGCGGCCGA Similarity nucleic acid Seidman, 7175 base pairs (619)238-0062 Conservative FastSEQ Version 1.5 IBM Compatible 6855..7175 1..143 5'UTR 144..6857 linear (619)238-0999 Diskette 04-APR-1989 DNA (genomic) JMBER: US 07/620,250 30-NOV-1990 double Stephanie L 3.8%; us 07/176,899 WO PCT/US89/01408 US 07/603,751 US 07/482,384 07/868,354 52516 0; Score 49; DB 2; Length 7175; Pred. No. 0.0094; Mismatches (P519739) 215; Gap 2857

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07
FILING DATE: 13-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 10-APR-1992
                                                                                                                                               PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/482,384
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PO
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
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TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 40
                  PRIOR APPLICATION DATA:
                                                                 PRIOR APPLICATION DATA:
US 07/603,751
                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 30-NOV-
                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/105,536
FILING DATE: 11-AUG-1993
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CURRENT APPLICATION DATA:
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                                                                                                                                     APPLICATION NUMBER: US 0'FILING DATE: 20-FEB-1990
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                                 APPLICATION NUMBER: WO PUT FILING DATE: 04-APR-1989
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1660 Union Street
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Feldman, Daniel
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30-NOV-1990
                                                                                     04-APR-1989
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                                                  WO PCT/US89/01408
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US 07/176,899
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                                                                                                                             Patent No. 6090623
GENERAL INFORMATION:
APPLICANT: Harpol
                                                                                                                                                                              Sequence 8,
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Best Local Similarity
Matches 201; Conserv
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            APPLICANT: McCue, Ann
APPLICANT: Gillespie, Alisor
TITLE OF INVENTION: HUMAN CJ
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 38
                                                                                                APPLICANT:
                                                                                                                                                                                                                                                           3048 GCGGAGAGCGGGGAGGAGCCGGCGCGCGCACCGGGCACAAGGCGCAGCCTGCT 3107
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CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                           610 GGGCAGGCCGGGTGGGAGCAGCAGCCACCGGAGGACCGGAACAGTGTGGCGGCGAT 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                         550 GTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCAGGCTGCA 609
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REGISTRATION NUMBER: 33,779
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                                                                                                                                                                              Application US/08949386
                                                         McCue, Ann
Gillespie, Alison
                                                                                              Harpold, Michael
Ellis, Steven
Williams, Mark
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                                             CALCIUM CHANNEL COMPOSITIONS AND
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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NAME: Seidman, Stephanie
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                                2988 GCCGCCAAGGGCGAGCGGCGCGCGCGCACCGGGGCCCCCGAGCGGGGCCCCCGGGAG 3047
                                                                                                                                                           2868 GGCCCAGGCCCCGAGGGCGGCCGGCGGCACCACCGGCGCGCGCTCCCCGGAGGAGGCGGCC 2927
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                                                                                              2928 GAGCGGGAGCCCCGACGCCACCGCGCGCACCGGCACCAGGATCCGAGCAAGGAGTGCGCC 2987
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                                                              490, CCCACGAAGGGAAGAGGGGAGCCCGGCATCCTCGGGGAACCCGGGAACCGGAGCCGAGAGAG 549
                                                                                                                            370 CCCCGTGGCCACGCCGGCGCGGGAGATCCCCGCGATCCTGGCAGACCGTAGCCCCGTTC 429
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STREET: 16
 550 GTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCAGGCTGCA 609
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LOCATION:
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APPLICATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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1660 Union Street
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                                                                                                                                                                                                                                                                                                                                                   Conservative
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Pred. No. 0.0094;
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      PRIOR APPLICATION DATA: APPLICATION NUMBER:
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RESULT 12
US-08-450-562-8
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APPLICANT:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/4
FILING DATE: 13-MAR-1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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                                                                 PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                     5-NOV-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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                                    13-JULY-1992
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   07/868,354
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10-APR-1992

PCT/US92/06903

PRIOR APPLICATION DATA:

FILING DATE:

14-AUG-1992

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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
FRUGTH: 7175 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0999
                                                                                                2988 GGCGCCAAGGGCGAGCGGCGCGCGCGCACCGCGGCGCCCCCGAGCGGGGCCCCCGGGAG 3047
                                                                                                                                                               2928 GAGCGGGAGCCCCGACGCCACCGCGCGCACCAGGATCCGAGCAAGGAGTGCGCC
                                                                                                                                                                                                                              2868 GGCCCAGGCCCGAGGGCGGCCGGCGCACCGGCGCGCGCTCCCCGGAGGAGGCGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 04-APR-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 02-FEB-1990 PRIOR APPLICATION DATA:
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610 GGGCAGGCCGGGTGGGAGCAGCAGCCACCGGAGGACCGGAACAGTGTGGCGGCGAT 668
                                                             550 GTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGGGGGGATGTTCAGGCTGCA 609
                                                                                                                             490 CCCACGAAGGGGAGAGCCCGGCATCCTCGGGGACCCGGGAACCGGAGCCGAGAGAG 549
                                                                                                                                                                                                   430
                                                                                                                                                                                                                                                           370 CCCCGTGGCCACGCCGGCGGGGGGAGATCCCCGGGATCCTGGCAGACCGTAGCCCCGTTC 429
                                                                                                                                                                                                                                                                                                                            310 CGCACGCTGCAGCCTGCAGGGTGCCGAGCCCAGCCCCGACGCCCGATCGGGTTCCTGTCAA 369
                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/603,751 FILING DATE: 08-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07/620,250 FILING DATE: 30-NOV-1990
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                                                                                                                                                                                                                                                                                             201;
                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity 48.0%;
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RATION NUMBER: 33,779
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1..143
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                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                Matches 201;
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Best Local Similarity
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GENERAL INFORMATION:
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                          2868 GGCCCAGGCCCGAGGGCGGCGGCGCACCACCGGCGGCGCTCCCCGGAGGAGGCGGCC 2927
                                                                                                                                                2811
                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (619) 450-8400
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ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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370 CCCCGTGGCCACGCCGGCGCGCGGAGATCCCCGCGATCCTGGCAGACCGTAGCCCCGTTC 429
                                                                                                                310 СССАСССТССАСССТССАСССТВССССВАССССВАСССССВАТССВСТТСФТСТСАА 369
                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                          250 GACGCTGCGGTGCAGGTGAACCCGCGCGCGCGACGCCTCGGTGCAGTGTTCACTCGGGCGC 309
                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
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OPERATING SYSTEM:
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REFERENCE/DOCKET NUMBER: 24
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (619) 587-5360
                                                                                                                                                                                                              Conservative
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1..143
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                                                                                                                                                                                                                                                                                                                                                                              144..6857
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N: 435
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                                                                                                                                                                                                                           3.8%;
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Pred. No. 0.0094;
0; Mismatches 215; Indels
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                             FILING DALL:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/193,078
APPLICATION NUMBER: 07-FEB-1994
                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: 08/311,363
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/404,950
FILING DATE: 13-MAR-1995
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APPLICANT:
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              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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CITY: S
                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/31 FILING DATE: 23-SEPT-1994
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/336,257 FILING DATE: 7-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                       APPLICATION NUMBER: 08/223,305
                                                                                                                                                                                                           APPLICATION NUMBER:
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APPLICATION NUMBER:
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VENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gillespie, Alison
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Ellis, Steven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                         11-AUG-1994
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08/149,097
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Best Local Similarity
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APPLICATION NUMBER:
FILING DATE: 15-AUG-
3048 GCGGAGAGCGGGGAGGAGCCGGCGCGCGCACCGGGCCCGGCACAAGGCGCAGCCTGCT 3107
                                                                                                                               2928 GAGCGGGAGCCCCGACGCCACCGCGCACCGGCACCAGGATCCGAGCAAGGAGTGCGCC 2987
                                                                                                                                                                                                   2868
                                                                                                                                                                                                                                                                 2811
                                                                                                                                                                                                                                                                                                                                 2751 GAGGCCCCGAAGGCGGAGAGCGGGGAGCCCGGTGCCCGGGAGGAGCGGCCGCCGCCGCAC 2810
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TELECOMMUNICATION INFORMATION:
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                  490 CCCACGAAGGGGAGGGGGAGCCCGGGCATCCTCGGGGACCCGGGAACCGGAGGCCGAGAGAG 549
                                                                                                                                                                370 CCCCGTGGCCACGCCGGCGCCGCGAGATCCCCGCGATCCTGGCAGACCGTAGCCCCGTTC 429
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LOCATION:
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14-AUG-1992
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48.0%;
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Gaps

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CURRENT APPLICATION NUMBER: US/09/268,163B
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: US 60/077,901
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 7177
TYPE: DNA
ORGANISM: Homo sapiens
Search completed: January 19, Job time : 134 secs
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US-09-268-163-7
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US-09-268-163-7
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APPLICANT: Lipscombe, Diane
APPLICANT: Schorge, Stephanie
APPLICANT: Schorge, Stephanie
TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
FILE REFERENCE: B1055/7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09268163B Patent No. 6353091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                             3050 GCGGAGAGCGGGAGCAGCCGGCGCGGCACCGGGCCCGGCACAAGGCCCAGCCTGCT 3109
                                                                                                                                                                                                                  2990 GGCGCCAAGGGCGAGCGCGCGCGCGCGCGCGCGCGCCCCGAGCGGGGCCCCGGGAG 3049
                                                                                                                                                                                                                                                                                         2930 GAGCGGGAGCCCCGACGCCACCGCGCACCGGCACCAGGATCCGAGCAAGGAGTGCGCC 2989
                                                                                                                                                                                                                                                                                                                                                                  2753 GAGGCCCCGAAGGCGGAGAGCGGGGAGCCCGGGTGCCCGGGAGGAGCGGCCGCGGCCGCAC 2812
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48.0%; Pred. No. 0.0094;
vative 0; Mismatches 215; Indels
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GenCore version 5.1.3 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 19, 2003, 19:49:35; Search time 62 Seconds (without alignments) 9183.449 Million cell updates/sec

US-09-844-864-1 1277

Perfect score:

Scoring table: IDENTITY_NUC

393868 seqs, 222934149 residues Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 100% Listing first 45 summaries

Database

ALIGNMENTS

Published_Applications_NA:*

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/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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US-09-860-846-1	US-09-894-998-35	US-09-795-686-104	US-09-795-668-104	US-09-946-807-104	US-10-033-026-3	US-10-033-026-5	US-09-954-456-1179	US-10-033-026-7	US-09-954-456-1601	US-09-844-864-24	US-09-844-864-20	US-09-844-864-23	US-09-844-864-19	US-09-844-864-25	US-09-844-864-21	US-09-844-864-22	US-09-844-864-18	US-09-844-864-1	ID
Sequence 1, Appli	Sequence 35, Appl	104	4	Sequence 104, App	ω `		Ξ		1601	24,	20,	23,	19,	Sequence 25, Appl	Sequence 21, Appl	Sequence 22, Appl	Sequence 18, Appl	Sequence 1, Appli	Description

; Sequence 1, Application US/09844864); Patent No. US20020042926A1 US-09-844-864-1 US-09-844-864-1 RESULT 1 GENERAL INFORMATION: SOFTWARE: PatentIn version 3.0 SEQ ID NO 1 PRIOR APPLICATION NUMBER: PCT/US99/25209 PRIOR FILING DATE: 1999-10-28 NUMBER OF SEQ ID NOS: 25 APPLICANT: Ren, Yongsheng
APPLICANT: Wu, Xuemei
APPLICANT: Wu, Xuemei
TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: P01925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT FILING DATE: 2001-04-27 PRIOR APPLICATION NUMBER: 60/106,020 PRIOR FILING DATE: 1998-10-28 APPLICANT: Matzuk, Martin LENGTH: 1277
TYPE: DNA
ORGANISM: Mus musculus

Q Ъ QΥ B В Q Matches 1277; Best Local Similarity Query Match 121 121 CGACCCGCGCCCCCCTCCTTCCTCCCCGGCTACAGACAGCTCATGGCCGCGGAGTACGTC 180 61 61 CATCCTTATCCGCAGGCCACAAAGCCGGGGATGGCTGGAGGTTCGGAGCCAGGGGCTGC 120 1 AAGGCGGGCGAGGCGCGGGACGCACCCATGTTCCCGGCGAGCACGCTTCCACCCCTGCCCC 60 CATCCTTATCCGCAGGCCACCAAAGCCGGGGGATGGCTGGAGGTTCGGAGCCAGGGGCTGC 120 AAGGCGGGCGAGGCGCGCACCCATGTTCCCGGCGAGCACGTTCCACCCCTGCCCG 60 Conservative 100.0%; Score 1277; DB 10; Length 1277; 100.0%; Pred. No. 2e-307; 7ative 0; Mismatches 0; Indels 0; 0; 0; Gaps

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                                                                                                                                                                                                                                                                    CCCTAAACGCCCCCATCGGCAAGACTTGTGTGGGAGATGCAAGGACAAACGCCTGTCCTG
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                           AAAAAAAAAAAAAAAA 1277
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APPLICANT: Matzuk, Martin
APPLICANT: Ren, Yongsheng
APPLICANT: Wu, Xuemei
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Best Local Similarity 99.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/106,020
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: PCT/US99/25209
PRIOR FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 25
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TYPE: DNA
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                                                                                                                               CCCGTTCTCGTCCGTGACCTTCTGTGGCCTCTCCTCCTCACTGGAGGTTGCGGGAGGCAG
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GGCTGCAGGGCAGGCCGGGTGGGAGCAGCCACCACCGGAGGACCGGAACAGTGTGGC
           GGCTGCAGGGCAGGCCGGGTGGGAGCAGCAGCCACCGCAGGGAGGACCGGAACAGTGTGGC
                                           GCAGACACCCACGAAGGGAGAGGGGAGCCCGGCATCCTCGGGGACCCGGGAACCGGAGCC
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; TYPE: DNA
; ORGANISM: mus musculus
US-09-844-864-22
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Best Local Similarity
Matches 778; Conserv
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Patent No. US20020042916A1
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APPLICANT: Wu, Xuemei
TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEILE REFERENCE: P01925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT FILING DATE: 2001-04-27
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APPLICANT: Ren, Yongshen
APPLICANT: Wu, Xuemei
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PRIOR FILING DATE: 1999-10-28
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               CCCGTTCTCGTGACCTTCTGTGGCCTCTCCTCCTCACTGGAGGTTGCGGGAGGCAG
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CCCGTTCTCGTCCGTGACCTTCTGTGGCCTCTCCTCCTCACTGGAGGTTGCGGGAGGCAG
                                                               CTGTCAACCCCGTGGCCACGCCGGCGCCGGGAGATCCCCGCGATCCTGGCAGACCGTAGC
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APPLICANT: Ren, Yongsheng
APPLICANT: Wu, Xuemei
TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: PO1925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT FILING DATE: 2001-04-27
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LENGTH: 305
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PRIOR APPLICATION NUMBER: 60/106,020
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: PCT/US99/25209
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                                                         1205 CATGACAGACAGTGTTACTTGGATATAAAGCCTGTGAATAAAAGGTATTGCAAACA 1260
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250 CATGACAGACAGTGTTACTTGGATATAAAGCCTGTGAATAAAAGGTATTGCAAACA 305
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95.3%;
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Pred. No. 8.1e-59;
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US-09-844-864-25
                                       SOFTWARE: PatentIn version 3.0
SEQ ID NO 19
LENGTH: 123
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 25
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APPLICANT: Ren, Yongsheng
APPLICANT: Wu, Xuemei
TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: P01925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 05/0166,020
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APPLICANT: Matzuk, Martin
APPLICANT: Ren, Yongsheng
APPLICANT: Wu, Xuemei
TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: P01925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 60/106,020
PRIOR FILING DATE: 1998-10-28
PRIOR FILING DATE: 1998-10-28
                                                                                                     PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: PCT/US99/25209
PRIOR FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 25
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PRIOR FILING DATE: 1999-10-28
ORGANISM: mus musculus
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Pred. No. 1.5e-55;
0; Mismatches 9; Indels 0;
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                  SEQ ID NO 20
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Patent No.
                                                                                                                          APPLICANT: Matzuk, Martin
APPLICANT: Ren, Yongsheng
APPLICANT: Wu, Xuemei
APPLICANT: Wu, Xuemei
TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: P01925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 60/106,020
PRIOR FILING DATE: 1998-10-28
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APPLICANT: Ren, Yongsheng
APPLICANT: Wu, Xuemei
                                          SOFTWARE: PatentIn version 3.0
                                                             PRIOR FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 25
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SOFTWARE: PatentIn version 3.0
                                                                                   PRIOR APPLICATION NUMBER: PCT/US99/25209 PRIOR FILING DATE: 1999-10-28
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PRIOR FILING DATE: 1999-10-28
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LENGTH: 105
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Local Similarity 98.0%;
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98.0%;
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Pred. No. 1.3e-15;
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PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR PRIOR PRIOR NUMBER: US/60/234,052
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR APPLICATION NUMBER: US/60/235,637
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LENGTH: 105
                                                                                                                                                                   APPLICANT: Young, Paul TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc TITLE OF INVENTION: Sets FILE REFERENCE: 689290-76 CURRENT APPLICATION NUMBER: US/09/954,456 CURRENT FILING DATE: 2001-09-18
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FILE REFERENCE: P01925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 60/106,020
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: PCT/US99/25209
PRIOR FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 25
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Patent No. US20020042926A1
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Matches 72; Conservative
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US-10-033-026-7
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PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/077,901
PRIOR FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
Matches 201; Conserv
                                           Query Match
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Best Local Similarity
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LENGTH: 14800
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CURRENT FILING DATE: 2001-12-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lipscombe, Diane
APPLICANT: Schorge, Stephanie
TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/268,163 PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: B1055/7000
                                                                                                            NAME/KEY: CDS
LOCATION: 146
                                                                                                                                                            FEATURE:
                                                                                                                                                                               ORGANISM: Homo sapiens
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                                                                                                                                                                                                       TYPE: DNA
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ORGANISM: Homo sapiens
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                Score 49; DB 12; Length 7177; Pred. No. 0.016;
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                                                                                                    ; ORGANISM: Homo sapiens US-09-954-456-1179
                                                                                                                                                                     SOFTWARE: PatentIn version 3.0
SEQ ID NO 1179
LENGTH: 7364
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                                                       Query Match
Matches 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
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PRIOR APPLICATION NUMBER: US/60/234, 923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235, 134
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
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                                                                                                                                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US/60/235,863
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                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US/60/235,720
                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
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                                    / Match 3.8%;
Local Similarity 48.0%;
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                                                                                                                                                                                                                                                                   2000-09-27
                Score 49; DB 10
Pred. No: 0.016;
0; Mismatches 2
                                                            DB 10; Length 7364;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 5
LENGTH: 7364
                                                                                                                                                                                                                                                                                                                                                Query Match 3.8%; Score 49; DB 12; Length 73
Best Local Similarity 48.0%; Pred. No. 0.016;
Matches 201; Conservative 0; Mismatches 215; Indels
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CURRENT APPLICATION NUMBER: US/10/033,026
CURRENT FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 09/268,163
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: US 60/077,901
PRIOR EILING DATE: 1998-03-13
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APPLICANT: Schorge, Stephanie
TITLE OF INVENTION: HUMAN -TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
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SOFTWARE: FastSEQ for Windows Version 3.0
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LOCATION: 146..7162
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                                                                                                                                                                  2813
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                                                                      2870 GGCCCAGGCCCCGAGGGCGGCCGGCGGCACCACCGGCGCGGCTCCCCGGAGGAGGCGGCC
                                                                                                                                                                                                      310 CGCACGCTGCAGCCTGCAGGGTGCCGAGCCCAGCCCCGACGCCCGATCGGGTTCCTGTCAA 369
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370 CCCCGTGGCCACGCCGGCGCGCGGGAGATCCCGCGATCCTGGCAGACCGTAGCCCCGTTC 429
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; LOCATION: 146..7174
US-10-033-026-3
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Best Local Similarity
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CURRENT FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 09/268,163
PRIOR ETLING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: US 60/077,901
PRIOR FILING DATE: 1998-03-13
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TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
FILE REFERENCE: B1055/7000
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                                      GGGCAGGCCGGGTGGGAGCAGCAGCCACCGGAGGACCGGAACAGTGTGGCGGCGAT 668
                                                                             GCGGAGAGCCGGGAGGAGCCCGCGCGCGCGCACCACCGGGCACAAGGCGCAGCCTGCT
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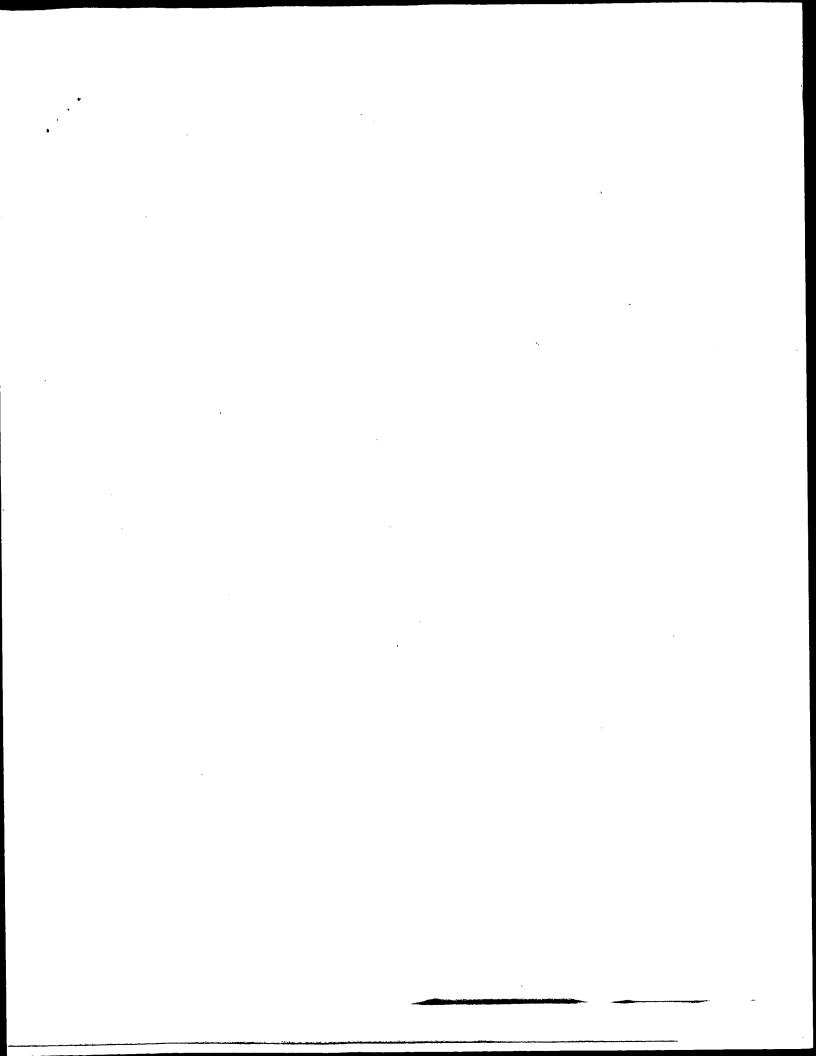
Search completed: January 19, Job time: 88 secs

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; ORGANISM: Homo sapiens
US-09-946-807-104
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US-09-946-807-104/c
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Best Local Similarity 44.9%;
Matches 217; Conservative
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TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Stefansson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
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278 GCG
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                                                                                   338 GAGCGGGCGGAGCCGGGGCGCTGGGCCCGGGGGCCCGGGACGCCCGGAGCGCGCGGG
                                                                                                                        598 GTTCAGGCTGCAGGGCAGGCCGGGTGGGAGCAGCAGCAGCACCACCGGAGGACCGGAACAGT 657
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Pred. No. 0.027;
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                 28-OCT-1998;
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                                                                          28-OCT-1999;
                                                                                                   04-MAY-2000.
                                                                                                                                                                                                               Mus sp.
                                                                                                                                                                                                                                                                                    Mouse oocyte-specific 01-180 cDNA clone.
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/product= "Mouse oocyte-specific protein, Ol-180"
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                                                                                                                                              acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer;
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pulmonary vasoconstriction; inflammation; allergic rhinitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX55272-74. These multiple target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYEC-) UNIV EAST CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 TCCTTATCCGCAGGCCACCAAAGCCGGGGATGGCTGGAGGTTCGGAGCCAGGGGCTGCCG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GGCGGGCGAGGCGCACCCACCCATGTTCCCGGCGAGCACGTTCCACCCCTGCCCGCA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rocar
GGCCGGGCCGSNNNDNNGCCBGGGCGCGCCGCCGGCCGGCCGGSNNNDNNCCBGGGCGCG 10511f
                                               GCCCCGTTCTCGTCCGTGACCTTCTGTGGCCTCTCCTCCTCACTGGAGGTTGCGGGAGGC
                                                                                                                                                                                                                                                                                                                                               CAGCCGTGACGCTGCGGTGCAGGTGAACCCCGCGCGC--GACGCCTCGGTGCAGTGTTCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                GSNNNDNNBGGCCBGGGGGGGCGGCCGGCCGGGCCGSNNNDNNGGCCBGGGCGCGCGCC
                                                                                                                                             TCCTGTCAACCCCGTGGCCACGCCGGCGCGCGGGAGATCCCCGCGATCCTGGCAGACCGTA 420
                                                                                                                                                                                               CCBGGGCGCGGCCGGGCCGGGCCGSNNNDNNCBGGCCBGGGCGGCGGCCGGCCGGCCGGCC
                                                                                                                                                                                                                                              CTCGGGCGCCGCACGCTGCAGCCTGCAGGGTGCCGAGCCCAGCCCCGACGCCCGATCGGGT
                                                                                                                                                                                                                                                                                                                                                                                                 SNNNDNNCCGCBGGCCBGGSNNNDNNCCGCBGGCCBGSNNNDNNCCGCBGGCCBSNNNDN 104876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1999-229400/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0093972.
97US-0059160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.6%; Score 58.8; DB 20; Length 32.6%; Pred. No. 0.0013; itive 71; Mismatches 441; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 114955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Gaps
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AAX53491/c
ID AAX534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105117 CCGCCGGCCGGGCCGSNNNDNNCBGGGCGCGCCCC--CGGCCGGGCCGSNNNDNNBGGGC 105174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105175
     The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides
                                                                                                                                           Disclosure; Page 37; 120pp; English.
                                                                                                                                                                                vasoconstriction
                                                                                                                                                                                           New antisense oligonucleotides used in treatment of,
                                                                                                                                                                                                                                WPI; 1999-229400/19
                                                                                                                                                                                                                                                                                                                                    09-JUN-1998;
17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukenia; lymphoma; carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human adenosine Al receptor antisense oligonucleotide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX53491 standard; DNA;
                                                                                                                                                                                                                                                                                                 (UYEC-) UNIV EAST CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9913886-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     colon cancer; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense oligonucleotide; multiple target; antisense treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 AGGCAGACACCCACGAAGGGAGAGGGGAGCCCGGCATCCTCGGGGAACCCGGGAACCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACCCCGGTGATTCGGATGCCCCTCGAGACCAGGCCTCCCCGCAAAGCACG
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97US-0059160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lung cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВР
                                                                                                                                                                                         e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               540
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sequences AAX55272-74.

These multiple target

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110999 GCGCGAGCGCNNHNNNSCGCCGGCAAGAGGGGCCCGGACCGCGGCAGCCCNNHNNNSCCC
                                                                                                                                                                                            110459 CGGGGCCCCNNHNNNSGGCGCGGGGGCCCCNNHNNNSCGGCGCGGGGCCCCNNHNNNSGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110759
                                                                                                                                                                                                                                                                                         110579 GGGCGGCGCGGGNNHNNNSGGCGGGCGGCGCGGGGNNHNNNSGGCGGGCGCGCGGGGCN 110520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110639 GGGCGGCGNNHNNNSGGCGGGCGCGNNHNNNSGGCGGCGGCGCGGNNHNNNSGGC 110580
110339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oligonucleotides (specifically AAX55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or have metastasized to the lungs, including breast and prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189
                                             728 GTGATTCGGATGCCCCTCGAGACCAGGCCTCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249
                                                                                                                                                                                                                                          608 CAGGGCAGGCCGGAGCAGCAGCCACCACCGGAGGACCGGAACAGTGTGGCGGCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 GCGCGGGACGCACCCATGTTCCCCGGCGAGCACGTTCCACCCCTGCCCGCATCCTTATCCG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    CACCCACGAAGGGAGGGGAGCCCGGCATCCTCGGGGACCCGGGAACCGGAGCCGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACCCCGTGGCCACGCCGGCGCGCGGAGATCCCGCGATCCTGGCAGACCGTAGCCCCGT 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACGGCGACGCCNNHNNNSGGGCCCGGGCCCVGCCGCCCCCCCCNHNNNSCCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNNHNNNSCGCGCCCGGCVCGCVGVVGCCCGCGCNNHNNNSGCGCGAGCCCGACVGGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCGCCCGGCCCCGCGGAGNNHNNNSTCGCCGGAGCCGCCGCGCAGCCAGCCCNNHNN 110880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCTCCTTCCTCCCC----GGCTACAGACAGCTCATGGCCGCGGAGTACGTCGACAGCCA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCCCCGCGCGCCCCNNHNNNSGGCGGGCGCCNNHNNNSGGCGGGCGGCGNNHNNNSGGC 110640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCGCACGCTGCAGCCTGCAGGGTGCCGAGCCAGCCCCGACGCCCGATCGGGTTCCTGTC 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGACGCTGCGGTGCAGGTGAACCCGCG-CCGCGACGCCTCGGTGCAGTGTTCACTCGGGC 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGCCACCAAAGCCGGGGATGGCTGGAGGTTCGGAGCCAGGGGGCTGCCGACCCGCGCCCC 132
  NHNNNSCGGGCGGCGCGCGCCCNNHNNNSGCGG
                                                                                                                                          TGCAGTCTGAGCCTGGGAGCGAGGAGCCATGTCCTGCCGCAGAGATGGCTCAGGACCCCG 727
                                                                                             GCGCGGGGCCCCNNHNNNSGGCGGCGCGCGGGCCCCNNHNNNSGGGCGGCGCGCGGGCCCCCN 110340
                                                                                                                                                                                                                                                                                                                                       AGGTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCAGGCTG
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Pred. No. 0.054;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 20; Length 114955;
     110305
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RESULT 4

AAV44436 ID AAV4

AAV44436

standard; DNA; 400

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                     20
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                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                        tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tuberculosis; immunogenic; soluble; antigen; p.
vaccine; pharmaceutical; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M. tuberculosis immunogenic polypeptide XP22 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV64545;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium
                                                                                                                                                                                                                                                                                                         Sequence 400 BP; 74 A; 151 C; 162 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 175; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA to develop products for the detection of M. tuberculosis infecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-261042/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-1998.
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                                                                                                                             578
                                                                                                                                                      179
                                                                                                                                                                                                                              458 CCTCACTGGAGGTTGCGGGAGGCAGGCAGGACACCCACGAAGGGAAGAGGGGAGCCCGGCAT 517
                                                                                                   239
                                                                                                                                                                               518
359
                      698 GTCCTGCCGCAGAGATGGCTCAGG 721
                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                       CTTCACCCAAGGCGCCGACGGCAACGCCGGCAACGCGGTGACGGCGGGGTCGGCGGCAA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SG,
                                                                                                                                                     CACCGGAGGACCGGAACAGTGTGGCGGCGATGCAGTCTGAGCCTGGGAGCGAGGAGCCAT
                                                                                                                                                                            CCTCGGGGACCCGGGAACCGGAGCCGAGAGAGGTGGCCGCGAGGAAAGCGGTCCCCCAGC 577
CGGCGGCGACGGTGCACTCTCAGG
                                                                                                  CGCGAAGCGAGGGGGATGTTCAGGCTGCAGGGCAGGCCGGGTGGGAGCAGCAGCCAC
                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Skeiky YAW,
                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0818112.
96US-0730510.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dillon DC, Houghton
Y YAW, Twardzik DR,
                                                                                                                                                                                                                                                                      3.9%;
49.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Houghton R,
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                                                                                                                                                                                                                                                                      Score 49.6; DB Pred. No. 0.033;
                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                    DB 19; Length 400;
                                                                                                                                                                                                                                                          134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis infection
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                                                                                                                                                                                                                                                           Indels
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences. The invention relates to methods and compositions for diagnosing tuberculosis. It provides polypeptides (see AAM64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of a M. tuberculosis antigen, or an immunogenic portion of a M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using the composition of the patient with the patient with the composition of the patient with the composition of the patient with the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic DNA expression library using sera from patients having extrapulmonary tuberculosis. It bears no similarity to known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the 5' region of DNA coding for an antigenic portion of Mycobacterium tuberculosis antigen XP22; 3' DNA is provided in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated Mycobacterium tuberculosis polypeptides and to develop products for the detection of M. tuberculosis and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 400 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        these polypeptides, antibodies or oligonucleotide probes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV44437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 185-186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-251292/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-1997;
11-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-1998
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698 GTCCTGCCGCAGAGATGGCTCAGG 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                         CCTCGGGGACCCGGGAACCGGAGAGCCGAGAGAGGTCGCCGAGGC 577
                                                                                                                                                                                                                                                                                                                           CTTCACCCAAGGCGCCGACGGCAACGCCGGCAACGGCGGTGACGGCGGGGTCGGCGAA 178
                                                                                      CACCGGAGGACCGGAACAGTGTGGGGGCGATGCAGTCTGAGCCTGGGAGCGAGGAGCCAT 697
                                                                                                                                                                                XP22 DNA was isolated from a M. tuberculosis strain Erdman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection; diagnosis; antigen; xP22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0818111
96US-0729622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 A; 151 C; 162 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.9%;
49.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain Erdman
                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49.6; DB Pred. No. 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Houghton R,
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                         134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    intection
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AAZ19346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                         Matches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                    Best
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical composition or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretin by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAY39083 to anvagors are used in the account of the containing the part of the containing the contai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Campos-Neto A,
Lodes MJ, Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 400 BP; 74 A; 151 C; 162 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY39225 are used in the exemplification of the present invention
                                                         638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 170; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-FEB-1999;
            299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M. tuberculosis antigen 5' XP22 DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ19346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ19346 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune response; skin test; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunotherapy; diagnosis; immunisation; vaccine; infection;
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                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                          CACCGGAGGACCGGAACAGTGTGGCGGCGATGCAGTCTGAGCCTGGGAGCGAGGAGCCAT
                                                                                                                                                                                                                                                                                CTTCACCCAAGGCGCCGACGGCAACGCCGGCAACGGCGGTGACGGCGGGGGTCGGCGGCAA 178
                                                                                                                                                                                                                                                                                                                               CCTCACTGGAGGTTGCGGGAGGCAGGCAGGACACCCACGAAGGGAAGGGGGAGCCCGGCAT 517
CCTCGGGGACCCGGGAACCGGAGCCGAGAGAGGTGGCGGGGGAAAGCGGTCCCCCAGC 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1999-527409/44.
                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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98US-0025197
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                                                                                                                                                                                                                                                                                                                                                                                                          3.9%;
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                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 134; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 400;
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Best Local :
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                                                                                                                                                                                                                                                                                                                  This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigen;
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                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 215-216; 323pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-527416/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAY-1998;
18-FEB-1998;
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                                                                                                                                                                                                                                                                                Sequence 400 BP; 74 A; 151 C; 162 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                        current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide comprising antigenic portions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
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698 GTCCTGCCGCAGAGATGGCTCAGG 721
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                                                                                                                                                                                                         458 CCTCACTGGAGGTTGCGGGAGGCAGGCAGACACCCACGAAGGGAGAGGGGGAGCCCGGCAT 517
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                                                                                                                                                                                                                                            Local Similarity
                                                         CACCGGAGGACCGGAACAGTGTGGCGGCGATGCAGTCTGAGCCTGGGAGCGAGGAGCCAT 697
                                                                                                                                                                                  CTTCACCCAAGGCGCCGACGGCAACGCCGGCAACGGCGGTGACGGCGGGGTCGGCGAA 178
                                    CGCGAAGCGAGGAGGCGATGTTCAGGCTGCAGGGCAGCCGGGTGGGAGCAGCCAC
                                                                                                                                   CCTCGGGGACCCGGGAACCGGAGCCGAGAGAGGTGGCCGCGAGGAAAGCGGTCCCCCAGC
                                                                                    130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reed SG,
                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tuberculosis.
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98US-0024753.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombinant antigen DNA encoding 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS.
                                                                                                                                                                                                                                          3.9%;
49.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skeiky YAW,
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YAW, Twardzik DR,
                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                          Score 49.6;
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                                                                                                                                                                                                                                   Indels
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                                                                                                                                                             577
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RESULT 8
ABL66291
  В
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18-SEP-2000;

18-SEP-2000;

20-SEP-2000;

20-SEP-2000;

22-SEP-2000;

25-SEP-2000;

26-SEP-2000;

27-SEP-2000;

27-SEP-2000;

28-SEP-2000;

28-SEP-2000;

29-SEP-2000;

28-SEP-2000;

28-SEP-2000;

29-SEP-2000;

28-SEP-2000;

29-SEP-2000;

20-SEP-2000;

20
                                                                                                                                                      03-OCT-2000;
03-OCT-2000;
03-OCT-2000;
03-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL66291 standard; DNA; 14800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lung cancer related gene sequence SEQ ID NO:4628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL66291;
Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2001; 2001WO-US10838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-DEC-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359 CGGCGGCGACGGTGCACTCTCAGG 382
                                                         (AVAL-) AVALON PHARM.
                  Augustus M,
                                                                                                                                                                                                                                                                                                                                                  2000US-234509P

2000US-23457P

2000US-234924P

2000US-235077P

2000US-235082P

2000US-235134P

2000US-235638P

2000US-235638P

2000US-235638P

2000US-235721P

2000US-235721P

2000US-235840P

2000US-235840P

2000US-236840P

2000US-236032P

2000US-236032P

2000US-236032P

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2000US-236032P

2000US-236032P

2000US-236034P

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2000US-236034P
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2000US-233617P.
2000US-234009P.
                                                                                             2000US-237606P.
2000US-237608P.
2000US-244867P.
2000US-245084P.
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2000US-237316P.
2000US-237425P.
  Weaver Z;
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2000US-234052P.
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                                                                                                                                                                           2000US-237598P.
2000US-237604P.
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2000US-237173P.
                      Carter KC,
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                      Ebner R,
                        Endress G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in agent to be tested for anti-neoplastic activity, determining a change in agent to the tested for anti-neoplastic activity, determining a change in agent of a signature gene set, where (I) accomprises a sequence (S) selected from 8447 sequences (given in ABL51664 to ABL70110), or is at least 95% identical to (S), where a change in accomprises in indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical accompanies of the agent. MI can be used in the adeas collent because in the convey the chemical consequence overlan, kidney, prostate, stomach, lung, thyroid, adeance of the agent and can be used in the consequence accompanies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 139;
                                                                                                                              Human; foam cell differentiation; atherosclerosis; cerebral stroke; cardiovascular disorder; coronary artery disease; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4182
               18-OCT-2001
                                                        WO200177389-A2
                                                                                                Homo sapiens.
                                                                                                                                                                                               Human DNA sequence #113 expressed during foam cell differentiation
                                                                                                                                                                                                                                               14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                  AAS94858 standard; DNA; 14835
                                                                                                                                                                                                                                                                                                                                                                                                                                          4302 GAAGGAGCTGCAGCAGCATGCAGGAGGAGGTGGTGCGGCGGGAGGAGGAGGCGGCGGTGGA 4361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14800 BP; 2890 A; 4567 C; 5319 G; 2024 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID 4628; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-188264/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                747 AGACCAGGCCTCCCCGCAAAGCACGGAGCAGGACAAGGAGCGCCTGCG 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         507 GAGCCCGGCATCCTCGGGGACCCGGGAACCGGAGCCGAGAGAGGTGGCCGCGAGGAAAGC 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGCAGCGGCAGCTGGCCGAGGCGACGCCCAGGCAAAGGCACAGGCGGAGCGGGAGGC 4301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCTGAGCAGCAGCGGGCAGAGCAGCGGCTGGCCGAGGTGGAGGCCGCGCTGGA 4241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCAGGCTGCAGGGCAGGCCGGGTGGGA 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGCCAGTACATCAAGTTCATCAGCGAGACTCTGCGGCGCATGGAGGAGGAGGAGGAGGAGGCT 4181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGAGGAGCCATGTCCTGCCGCAGAGATGGCTCAGGACCCCGGTGATTCGGATGCCCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.9%;
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Pred. No. 0.1;
0; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                    ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during foam cell differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be used in the diagnosis of disorders associated with foam cell development such as atherosclerosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotides sequences can also be used as PCR primers and probes. The polynucleotides of the invention are also polynucleotides of the invention are also polynucleotides equences of the invention which are differentially
                                          Calcium channel subunit; antagonist; agonist; diagnosis; Lambert Eaton Syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                            4269 GAAGCAGCGGCAGCTGGCCGAGGCGACGCCAGGCAAAGGCACAGGCGGAGGCGGAGGC
                                                                                                 Human neuronal calcium channel subunit alpha 18-2.
                                                                                                                                       01-DEC-1995
                                                                                                                                                                                                              AAQ84658 standard; DNA; 7175
                                                                                                                                                                                                                                                                                                4389 CGCGCAGCAGCAGCAGCAGCATTCAGGAGGAGCTGCAGCAGCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4149 GAGCCAGTACATCAAGTTCATCAGCGAGACTCTGCGGCGCATGGAGGAGGAGGAGGAGGCT 4208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polynucleotides that are differentially expressed in foam cell development -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14835 BP; 2881 A; 4568 C; 5306 G; 2018 T; 62 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expressed during foam cell differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 165-169; 315pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-APR-2001; 2001WO-US11128
                                                                                                                                                                                                                                                                                                                                   747 AGACCAGGCCTCCCCGCAAAGCACGAGCAGGACAAGGAGCGCCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          507 GAGCCCGGCATCCTCGGGGACCCGGGAACCGGAGCCGAGAGAGGGTGGCCGCGAGGAAAGC 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        CGAGGAGCCATGTCCTGCCGCAGAGATGGCTCAGGACCCCGGTGATTCGGATGCCCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTGAGCAGCAGCAGGAGGAGCGCGAGCGGCTGGCCGAGGTGGAGGCCGCGCTGGA 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCAGGCTGCAGGGCAGGCCGGGTGGGA 626
                                                                                                                                                                                                                                                                                                                                                                       GAAGGAGCTGCAGCAGCGCATGCAGGAGGAGGTGGTGCCGGCGGAGGAGGCGGCGGTGGA 4388
                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.9%;
48.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49.6;
Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seilhamer JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 14835;
                                                                                                                                                                                                                                                                                                    4436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC the human alpha 1B subunit was obtd. Nucleic acid amplification cC of specific regions of the IMR32 cell alpha 1B mRNA yielded additional segments of the alpha 1B coding sequence. A full-clent alpha 1B DNA clone was constructed by ligating portions cC length alpha 1B DNA clone was constructed by ligating portions cC of IMR32 cell RNA and genomic DNA using oligo primers corresp. to compare the partial cDNA clones. Nucleic acid amplification analysis cC of IMR32 cell RNA and genomic DNA using oligo primers corresp. to compare the subunit revealed an alternatively spliced alpha cC sequences located 5' and 3' of the stop codon of the DNA encoding cC IB-encoding mRNA in IMR32 cells. This second mRNA product is the cresult of differential splicing of the alpha 1B subunit transcript to include another exon that is not present in the mRNA corresp. The alpha 1B subunit encoded by a DNA sequence that was initially isolated. The alpha 1B subunit encoded by a DNA sequence contg. an additional consist referred to as alpha 1B-1 and given in AAQ84657/R71005. Following the sequence of the additional exon in calpha 1B-1 had alpha 1B-1 and alpha 1B-2 encodes exon in alpha 1B-1 had alpha 1B-1 and alpha 1B-2 encodes exon in alpha 1B-1 and alpha 1B-2 encodes exon in calpha 1B-1 had alpha 1B-2 encodes exon in alpha 1B-1 and alpha 1B-2 encodes exon in alpha 1B-1 and alpha 1B-2 encodes exon in alpha 1B-2 exon in alpha 1B-2 encodes exon in alpha 1B-2 encod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding the alpha 1B subunit was isolated by screening a human basal ganglia cDNA library with fragments of the rabbit skeletal muscle calcium channel alpha 1 subunit-encoding cDNA. A portion of one of the positive clones was used to screen an IMR32 cell cDNA library. Clones that hybridised to the basal ganglia probe were used to further screen an IMR32 cell cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding human calcium channel sub-unit(s) - used for developing prods. for studying calcium channels, e.g. for \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9504822-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         library to identify overlapping clones that in turn were used to screen a human hippocampus cDNA libary. A series of clones to span nearly the entire length of the nt. sequence encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-AUG-1993;
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  2868 GGCCCAGGCCCGAGGGCGGCCGGCGCACCACCGGCGCGCGCTCCCCGGAGGAGGCGGCC
                                                                                                                                                                                                              2751
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7175 BP; 1415 A; 2197 C; 2168 G; 1395 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
                                                                                                                                                                                                                                                                250 GACGCTGCGGTGCAGGTGAACCCGCGCGCGCGACGCCTCGGTGCAGTGTTCACTCGGGCGC 309
                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                           GAGGCCCCGAAGGCGGAGAGCGGGGAGCCCGGGAGGAGCGGCCGCGCGCAC 2810
                                                 CCCCGTGGCCACGCCGGCGCGGGAGATCCCCGCGATCCTGGCAGACCGTAGCCCCGTTC
                                                                                                        CGCACGCTGCAGCCTGCAGGGTGCCGAGCCCAGCCCCGACGCCCGATCGGGTTCCTGTCAA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1B-1 the alpha 1B-1 and alpha 1B-2 seuences are identical.
                                                                                                                                                                                                                                                                                                                       201;
                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                    Conservative
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93US-0149097.
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6633..7175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "identical to alpha 1B-1"
                                                                                                                                                                                                                                                                                                                                             3.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harpold MM,
                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                  Score 49; I
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mccue AF,
                                                                                                                                                                                                                                                                                                                                                                        DB 16; Length 7175;
                                                                                                                                                                                                                                                                                                                            215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams ME;
                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                      04-APR-1994;
04-APR-1988;
04-APR-1989;
04-APR-1989;
04-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2988
                                                                                                                                                                                                                                                                                                                                                                                                                                                             5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes the alpha-1B subunit of a human calcium channel. The present sequence is derived from alternative splicing of AAV42685. Calcium channels are membrane-spanning, multi-subunit protons.
                                                                                                                                                                                                                                                                                                                                                                                                                3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       characterisation; Lambert Eaton Syndrome; LES; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha-1B subunit; human; calcium channel; assay; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV42686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV42686 standard;
                                                Claim 1; Columns 91-106; 166pp; English.
                                                                    DNA encoding human calcium channel alpha 1B sub:unit protein - useful for recombinant production of the channel for screening its modulators, and diagnosis of Lambert Eaton Syndrome
                                                                                                                                                                                                                                 30-NOV-1990;
15-AUG-1991;
                                                                                                                                                                                                                                                                                                                               31-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                     11-AUG-1998.
                                                                                                                                                                                                                                                                                                                                                                            US5792846-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  430
                                                                                                                        P-PSDB;
                                                                                                                                                           Williams
                                                                                                                                                                       Brenner
                                                                                                                                                                                             (SIBI-) SIBIA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGCAGGCCGGGTGGGAGCAGCAGCCACCGGCGGAGCACCGGAACAGTGTGGCGGCGAT 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCGCCAAGGGGGGGCGCGCGCGCGCGCGCGCGCGCCCCGAGCGGGGCCCCGGGAG 3047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCAGGCTGCA 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGCGGGAGCCCCGACCGCGCGCGCACCGGCACCAGGATCCGAGCAAGGAGTGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGGAGAGCGGGGAGCCGGCGGCGGCGGCACCGGGCACAAGGCGCAGCCTGCT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCACGAAGGGGAGGGGGAGCCCGGGCATCCTCGGGGGACCCGGGAACCGGAGGCCGAGAGAG 549
                                                                                                                                    1998-456192/39.
                                                                                                                        AAW63142
                                                                                                                                                                       æ
                                                                                                                                                            ME;
                                                                                                                                                                        Ellis SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human calcium channel alpha-1B-1 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                              90US-0482384
90US-0620250
                                                                                                                                                                                                                                                                      89WO-US01408
                                                                                                                                                                                                                                                                                 88US-0176899
89US-0603751
                                                                                                                                                                                                                                                                                                        94US-0223305
                                                                                                                                                                                                                                                                                                                                95US-0455543
                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
6855..7175
                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
144..6857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                         Feldman DH,
                                                                                                                                                                        Harpold MM,
                                                                                                                                                                          McCue
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multi-subunit proteins

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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                             01-AUG-2000
 04-APR-1988;
                               25-MAY-1995;
                                                                                            US6096514-A.
                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                            Human; calcium channel; calcium channel subunit; diagnosis;
                                                                                                                                                                                                                                                                            Human calcium channel alphalB-2 subunit encoding DNA.
                                                                                                                                                                                                                                                                                                                   22-DEC-2000
                                                                                                                                                                                                                                                                                                                                                 AAA71704;
                                                                                                                                                                                                                                                                                                                                                                             AAA71704 standard; DNA; 7175 BP
                                                                                                                                                                                                                               Lambert Eaton Syndrome; calcium channel subunit alphalB-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2928 GAGCGGGAGCCCCACCGCCACCGCCACCGGCACCAGGATCCGAGCAAGGAGTGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2868 GCCCAGGCCCCGAGGGCGGCGCGGCACCACCGGCGCGCGCTCCCCGGAGGAGGCGGCC 2927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7175 BP; 1415 A; 2197 C; 2168 G; 1395 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eaton Syndrome (LES) can be used as a diagnostic for the disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the subunits can be alternatively spliced when transcribed, giving more than one form of the protein from the same transcript, each having slightly different properties. In addition, the reactivity of the alpha 1 subunit with IgG molecules from the serum of an individual with Lambert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complete calcium channel, can be used in assays for the detection and characterisation of compounds that modulate the channel. The DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            550 GTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCAGGCTGCA 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           490 CCCACGAAGGGAGAGGGGAGCCCGGCATCCTCGGGGAACCCGGGAACCGGAGCCGAGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       that allow controlled entry of calcium ions into cells. This leads to depolarisation events required for muscle contraction. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombinant subunit, when expressed with nucleic acids encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370 CCCCGTGGCCACGCCGGCGCGGGAGATCCCCGCGATCCTGGCAGACCGTAGCCCCGGTTC 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310 CGCACGCTGCAGCCTGCAGGGTGCCGAGCCAGCCCCGACGCCCGATCGGGTTCCTGTCAA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 GACGCTGCGGTGCAGGTGAACCCGCGCGCGCGACGCCTCGGTGCAGTGTTCACTCGGGCGC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGCAGGCCGGGTGGGAGCAGCAGCCACCACCGGAGGACCGGAACAGTGTGGCGGCGAT 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGGAGAGCGGGAGGAGCCGGCGCGCGCGCACCGGGCCCGGCACAAGGCGCAGCCTGCT 3107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCGCCAAGGGCGAGCGCGCGCGCGCGCACCGCGGCGCCCCGAGCGGGGCCCCCGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                (first entry)
88US-0176899
                            95US-0450562
                                                                                                                                                        144..6857
                                                                                                                                                                       Location/Qualifiers
                                                                                                                   /product= "calcium channel alphalB-2 subunit"
                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0.11;
0; Mismatches 215; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19; Length 7175;
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                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel isolated DNA molecule (I) comprising a sequence encoding a beta3-1 subunit of a human calcium channel. Nucleic acid probes comprising 14-30 contiguous nucleotides of beta_3 subunit encoding DNA are useful for isolation and cloning of calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that express heterologous calcium channel are useful for identifying compounds that modulate calcium channel activity and in assays for identifying agonists and antagonists of calcium channel activity in humans. Human calcium channel subunit or eukaryotic cells expressing the channel are useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This sequence encodes the human calcium channel alphalb-2 subunit which is
           3048
                                                              2988 GCCCCAAGGCCAGCGCCCCCCCGCCCCCCGCGCCCCCCAGCGGGCCCCCGGGAG 3047
                                                                                                                                                                                                                                                           Sequence 7175 BP; 1415 A; 2197 C; 2168 G; 1395 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-FEB-1990;
08-NOV-1990;
30-NOV-1990;
                                                                                                        490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human calcium channel beta subunit polynucleotides, useful for producing recombinant eukaryotic cells and for diagnosing Lambert Eaton
                                                                                                                                                                                                                          370 CCCCGTGGCCACGCCGGCGCGGGAGATCCCGGGATCCTGGCAGACCGTAGCCCCGTTC 429
                                                                                                                                                                                                                                                                                        310 CGCACGCTGCAGCCTGCAGGGTGCCGAGCCAGCCCCGACGCCCGATCGGGTTCCTGTCAA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example II; Column 113-128; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ellis SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                       250 GACGCTGCGGTGCAGGTGAACCCGCGCGCGCGACGCCTCGGTGCAGTGTTCACTCGGGCGC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SIBI-) SIBIA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                Loca
GCGGAGAGCGGGGAGGAGCCGGCGCGCGCGCACCGGGCACAAGGCGCAGCCTGCT 3107
                                                                                              CCCACGAAGGGAGAGGGGAGCCCGGCATCCTCGGGGAACCCGGGAACCGGAGCCGAGAGAG 549
                                                                                                                             GAGCGGGAGCCCCGACGCCACCGCCACCGCCACCAGGATCCGAGCAAGGAGTGCGCC 2987
                                                                                                                                                           GTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCAGGCTGCA 609
                                                                                                                                                                                           GCCCAGGCCCGAGGGGGGCGGCGGCACCACCGGCGGCGCTCCCCGGAGGAGGAGGCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-548230/50.
                                                                                                                                                                                                                                                                                                                                                                                                 201;
                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB10573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williams ME,
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-0193078.
94US-0223305.
94US-029012.
94US-0311363.
94US-0314083.
94US-0314083.
94US-0314083.
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90US-0603751.
90US-0620250.
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                                                                                                                                                                                                                                                                                                                                                                                                          3.8%; Score 49; DB 21; Length 7175; 48.0%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McCue AF,
                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 215; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harpold MM;
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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610 GGGCAGGCCGGGTGGGAGCAGCAGCCACCACCGGAGGACCGGGAACAGTGTGGCGGCGAT 668

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RESULT 13
AAV29059
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                            Qy
                                                            Matches
                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                              calcium channels are disclosed. Subunit proteins (see AMAY388-60), fusion proteins, antibodies, as well as assays to identify agents that modulate calcium channel activity are also provided. Such agents can be used to treat certain central nervous system disorders by altering calcium channel activity. Methods of diagnosing diseases associated with particular calcium channels, such as Lambert-Eaton syndrome, are disclosed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9811131-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calcium channel; human; central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human calcium channel alB subunit cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV29059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV29059 standard; cDNA; 7266 BP
                                                                                                                                                                                                                                                                                                                                                               human neuronal calcium channel. cDNA clones encoding the alB subunit, the a2d subunit (see AAV29060) and a b3 subunit (see AAV29061) have been isolated. These have been inserted into expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen ARS, Franco R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAR-1998
                                                                                                                                                                                                                                                        calcium upstake, indicating that the proteins expressed by the clones are capable of forming a functioning calcium channel.

Nucleic acids encoding the 3 subunits, as well as vectors, host cells and methods of isolating nucleic acids encoding related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding human neuronal calcium channel subunit(s) - useful for diagnosis of and treatment of central nervous system disorders, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lambert-Eaton syndrome; diagnosis;
 2699
                                                                                                                                                                                                                                                                                                                 and omega-conotoxin GVIA toxin sensitive potassium-stimulated
                                                                                                                                                                                                                                                                                                                                  vectors and are stably expressed in transformed cell lines transformed cells show omega-conotoxin GVIA binding activity.
                                                                                                                                                                                                                                                                                                                                                                                                         This cDNA clone codes for the alB subunit (see AAW37878) of the
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 18; Fig 1; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAW37878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMHP ) AMERICAN HOME PROD CORP
                                                                                                                   Sequence 7266 BP; 1433 A; 2249 C; 2173 G; 1411 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lambert-Eaton syndrome
                               250
                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1998-207325/18
GAGGCCCCGAAGGCGGAGAGCGGGAGCCCGGGAGGAGCGAGCGGCCGCGGCCGCAC 2758
                    GACGCTGCGGTGCAGGTGAACCCGGGGCGCGCGACGCCTCGGTGCAGTGTTCACTCGGGCGC 309
                                                            201;
                                                                           Similarity
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0713118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US16146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7105
                                                                           3.8%;

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                                                             0:
                                                                             Pred.
                                                                                           Score 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nervous system disorder;
                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapy;
                                                                               No.
                                                                             0.12;
                                                                                           DB 19; Length 7266;
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                                                                215;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                       The
                                                                Gaps
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RESULT 14
AAQ37817
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Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ37817 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2936 GGCGCCAAGGGCGAGCGCGCGCGCGCACCGCGGCGCCCCCGAGCGGGGCCCCCGGGAG 2995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2876 GAGCGGGAGCCCCGACGCCACCGCGCACCGGCACCAGGATCCGAGCAAGGAGTGCGCC 2935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence encoding the alpha 1B-1 human calcium channel subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ37817;
           DNA encoding the alpha 1B subunit was isolated by screening a human basal ganglia cDNA library with fragments of the rabbit skeletal muscle calcium channel alpha 1 subunit-encoding cDNA. A portion of one of the positive clones was used to screen an IMR32 cell cDNA library. Clones that hybridized to the basal ganglia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 CGCACGCTGCAGCCTGCAGGGTGCCGAGCCCGACGCCCGATCGGGTTCCTGTCAA 369
                                                                                                                                                  DNA encoding specific human calcium channel sub-units
                                                                                                                                                                                                                                                                                                                                                                                        W09304083-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lambert Eaton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human calcium channel subunit; diagnosis; agonist; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 CCCCGTGGCCACGCCGCGCGCGGAGATCCCCGCGATCCTGGCAGACCGTAGCCCCGTTC 429
DNA prove were used to further screen an IMR32 cell cDNA library
                                                                                               Disclosure; Page 111-120; 150pp; English.
                                                                                                                         diagnosing Lambert Eaton syndrome
                                                                                                                                                                               P-PSDB; AAR33549.
                                                                                                                                                                                               WPI; 1993-093936/11.
                                                                                                                                                                                                                         Williams ME;
                                                                                                                                                                                                                                       Brenner R,
                                                                                                                                                                                                                                                                (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC
                                                                                                                                                                                                                                                                                            15-AUG-1991;
10-APR-1992;
                                                                                                                                                                                                                                                                                                                                    14-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                              04-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      610 GGGCAGGCCGGGTGGGAGCAGCAGCCACCGCAGGAGCACCGGAACAGTGTGGCGGCGAT 668
                                                                                                                                      dentifying calcium channel agonists and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCAGGCTGCA 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGGAGAGCGGGGAGCCGGCGCGCGGCACCGGGCCCCGGCACAAGGCCGCAGCCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCACGAAGGGAGAGGGGAGCCCGGCATCCTCGGGGACCCGGGGAACCGGAGCCGAGAGAG 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ellis SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    syndrome; ss
                                                                                                                                                                                                                                                                                             91US-0745206.
92US-0868354.
                                                                                                                                                                                                                                                                                                                                    92WO-US06903
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 144..7163
                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                         Feldman DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7362
                                                                                                                                                                                                                                         Harpold MM,
                                                                                                                                                                                                                                          Mccue AF;

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RESULT 15
AAQ84657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
             WO9504822-A
                                                                          misc_feature
                                                                                                                       misc_difference
                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                            Calcium channel subunit; antagonist; agonist; diagnosis; Lambert Eaton Syndrome; ss.
                                                                                                                                                                                                                                                                           Human neuronal calcium channel subunit alpha 18-1.
                                                                                                                                                                                                                                                                                                             01-DEC-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                           AAQ84657 standard; DNA; 7362 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ84657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3048 GCGGAGAGCGGGGAGGAGCCGGCGCGCGCCACCGGCCACAAGGCGCAGCCTGCT ;107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to identify overlapping clones that in turn were used to screen a human hippocampus cDNA library. In this way, a sufficient series of clones to span nearly the entire length of the nucleotide sequence encoding the human alpha 1B subunit was obtained. PCR amplification of specific regions of the IMR32 cell alpha 1B mRNA yielded additional segments of the alpha 1B coding sequence. A full-length alpha 1B DNA clone was constructed by ligating portions of the partial cDNA clone was constructed by 11gating portions of the partial cDNA clones (see AAQ37817, AAQ37818). Alpha 1B-1 and alpha 1B-2 are derived by alternative splicing of the alpha 1B subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2988 GCCCCAAGGCCGAGCGCGCGCGCGCACCGCGGCGCCCCCGAGCGGGCCCCCGGGAG 3047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2928 GAGCGGGAGCCCCACCGCCACCGCGCACCGGCACCAGGATCCGAGCAAGGAGTGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2868 GCCCAGGCCCGAGGGCGGCGGCGGCACCACCGGCGCGCGCTCCCCGGAGGAGGCGGCC 2927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     610 GGGCAGGCCGGGTGGGAGCAGCAGCCACCAGCGGAGGACCGGAACAGTGTGGCGGCGAT 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7362 BP; 1446 A; 2276 C; 2214 G; 1426 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               490 CCCACGAAGGGAGAGGGGAGCCCGGCATCCTCGGGGACCCGGGAACCGGAGCCGAGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 GACGCTGCGGTGCAGGTGAACCCCGCGCGCGCGCGCTCGGTGCAGTGTTCACTCGGGCGC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 CCCCGTGGCCACGCCGGCGCGGGAGATCCCCGGGATCCTGGCAGACCGTAGCCCCGTTC 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 CGCACGCTGCAGCCTGCAGGGTGCCGAGCCCAGCCCCGATCGGGTTCCTGTCAA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCAGGCTGCA 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                              /*tage b
/label= additional exon wrt alpha 1B-2
6820..7362
                                                                                                                    /*tag= a
6633..6819
                                                                                                                                                     144..7163
                                     /note= "identical to alpha 1B-2"
                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 215; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 14; Length 7362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
2988 GGCGCCAAGGGCGAGCGCGCGCGCGCACCGGGGCGCCCCGAGCGGGGCCCCGGGAG
                                                                                                                                                                          2868 GGCCCAGGCCCCGAGGGCGGCCGCCGCCACCACCGGCGCGCCTCCCCGGAGGAGGCGGCC 292:
                                                                                                                                                                                                                                                             2751 GAGGCCCCGAAGGCGGAGAGCGGGGAGCCCGGGTGCCCGGGAGGAGGGGCGGCGGCGCAC 2810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7362 BP; 1445 A; 2278 C; 2214 G; 1425 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The alpha 1B subunit encoded by a DNA sequence contg. an additional exon is referred to as alpha 1B-1 and given in AAO84657/R71005, whereas the other form is referred to as alpha 1B-2 and is given in AAO84658/R71006. Following the sequence of the additional exon in alpha 1B-1 the alpha 1B-1 and alpha 1B-2 seuences are identical.
                                         490 CCCACGAAGGGGAGGGGGAGCCCGGCATCCTCGGGGACCCGGGAACCGGGAGGCCGAGAGAG 549
                                                                                                                                                                                                                                                                                                       310 CGCACGCTGCAGCCTGCAGGGTGCCGAGCCAGCCCCGACGCCCGATCGGGTTCCTGTCAA 369
                                                                                                                                                                                                                                                                                                                                                                                         250 GACGCTGCGGTGCAGGTGAACCCGCGCGCGCGACGCCTCGGTGCAGTGTTCACTCGGGCGC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 138-149; 285pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              obtaining agonists and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding human calcium channel sub-unit(s) - used developing prods. for studying calcium channels, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-090900/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAR71005
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05-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                            CCCCGTGGCCACGCCGGCGGGGAGATCCCCGCGATCCTGGCAGACCGTAGCCCCGTTC 429
                                                                                     GAGCGGGAGCCCCGACGCCACCGCGCACCGGCACCAGGATCCGAGCAAGGAGTGCGCC 2987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gillespie A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0105536
93US-0149097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.8%;
48.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harpold MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49; DB 16; Length 7362; Pred. No. 0.12; 0; Mismatches 215; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Williams ME;
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- Qy DЪ Qy
- Search completed: January 19, 2003, 10:25:45 Job time : 508 secs